

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 12, 2006, 06:19:19 ; Search time 37.5 Seconds

(without alignments)
11469.038 Million cell updates/sec

Title: US-10-782-570-1

Perfect score: 3939

Sequence: 1 gtgaatcaataataataa.....caaaactatgattattataa 2235

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q/cgn2_1/USPTO.spool_p/US10782570/runat_12012006_060222_7522/app_query.fasta_1.2375
-DB=PIR -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10782570 @CN 1 1 57 @runat_12012006_060222_7522 -NCPUS=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRSADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1159	29.4	1180	2	A26858 parasporal crystal
2	1158	29.4	1180	2	I39870 parasporal crystal
3	923.5	23.4	934	2	B29838 parasporal crystal
4	819	20.8	1136	1	US8881 parasporal crystal
5	706	17.9	659	2	S10228 parasporal crystal
6	691	17.5	652	2	I39811 parasporal crystal
7	688	17.5	1138	2	A48944 parasporal crystal
8	672	17.1	1160	2	I40589 parasporal crystal
9	655.5	16.6	1157	1	S49247 parasporal crystal
10	616.5	15.7	652	2	A27323 parasporal crystal
11	607	15.4	1228	2	S00873 parasporal crystal
12	588.5	14.9	719	2	I39815 insecticidal prote
13	585.5	14.9	719	2	I39814 insecticidal prote
14	585.5	14.9	719	2	S25383 parasporal crystal

15	576	14.6	1165	2	S11446 parasporal crystal
16	575	14.6	1178	1	US8SXH parasporal crystal
17	574	14.6	649	1	JH0261 parasporal crystal
18	563.5	14.3	719	2	I40590 cryV465 protein
19	562.5	14.3	1177	2	A49785 parasporal crystal
20	551	14.0	1154	2	S39536 parasporal crystal
21	540.5	13.7	1171	2	A37829 parasporal crystal
22	540.5	13.7	1171	2	I40572 parasporal crystal
23	538	13.7	1174	2	S32649 parasporal crystal
24	534.5	13.6	1176	2	A48970 parasporal crystal
25	530	13.5	618	2	S11445 parasporal crystal
26	526.5	13.4	655	2	JC7140 protoxin - Bacilli
27	522.5	13.3	823	2	S04181 parasporal crystal
28	519.5	13.2	1174	2	A42459 parasporal crystal
29	517.5	13.1	1160	2	S32647 parasporal crystal
30	514.5	13.1	1189	2	S00944 parasporal crystal
31	512	13.0	934	2	A2798 parasporal crystal
32	512	13.0	1176	2	JT0241 parasporal crystal
33	506	12.8	1176	2	JC2219 parasporal crystal
34	504	12.8	1172	2	S32689 parasporal crystal
35	502.5	12.8	1155	2	I39838 parasporal crystal
36	501	12.7	1176	2	A22617 parasporal crystal
37	501	12.7	1176	2	S02215 parasporal crystal
38	500	12.7	1156	2	S19306 parasporal crystal
39	491.5	12.5	1155	2	A26513 parasporal crystal
40	491.5	12.5	1155	2	JD0002 parasporal crystal
41	491.5	12.5	1156	2	A29125 parasporal crystal
42	491	12.5	1166	2	S32645 parasporal crystal
43	490.5	12.5	1155	2	S02134 parasporal crystal
44	486.5	12.4	1181	2	A41052 parasporal crystal
45	469.5	11.9	613	2	JC6033 mosquitocidal prot

ALIGNMENTS

RESULT 1

A26858
parasporal crystal protein cry4Aa1 - Bacillus thuringiensis subsp. israelensis
N:Alternate names: parasporal crystal protein cryIVA
C:Species: Bacillus thuringiensis subsp. israelensis
C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 05-Oct-2004
C:Accession: A26858; S48691
R:Ward, B.S.; Ellar, D.J.
Nucleic Acids Res. 15, 7195, 1987
A:Title: Nucleotide sequence of a Bacillus thuringiensis var. israelensis gene encoding
A:Reference number: A26858; MUID:88015571; PMID:2821500
A:Accession: A26858
A:Molecule type: DNA
A:Residues: 1-1180 <WAR>
A:Cross-references: UNIPROT:P16480; UNIPARC:UPI000016EA42; GB:Y00423; NID:G40351; PIDN:
A>Note: the authors translated the codon GCA for residue 308 as Thr
R:Nishimoto, T.; Yoshisue, H.; Ihara, K.; Sakai, H.; Komano, T.
FEBS Lett. 348, 249-254, 1994
A:Title: Functional analysis of block 5, one of the highly conserved amino acid sequencer
A:Reference number: S48691; MUID:94307434; PMID:7913448
A:Accession: S48691
A:Molecule type: DNA
A:Residues: 667-676 <NIS>
A:Cross-references: UNIPARC:UPI000017819A
C:Superfamily: Parasporal crystal protein
C:Keywords: delta-endotoxin

Alignment Scores:	5.5e-68	Length:	1180
Pred. No.:	1159.00	Matches:	283
Score:	54.55%	Conservative:	131
Percent Similarity:	37.29%	Mismatches:	281
Best Local Similarity:	29.42%	Indels:	64
Query Match:	2	Gaps:	25
DB:			

US-10-782-570-1 (1-2235) x A26858 (1-1180)

QY 13 AATAATAATGAATATGAGATTATCGATTCA-----AAGAATTATCTTATCCTCTTAAC 66


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Db 524 HisSerSerValAspProIyAsnThrIleTyThrHisLeuThrThrGlnIleProIa 543
Qy 1699 ATCAAGGTAACAGCTTTGATACAACTCTAAGGTAATGAAGGACCTGGTCATACAGGA 1758
Db 544 VallysAlaAsnSerLeuGlyThrAlaSerIysValValGlnGlyProGlyHisThrGly 563
Qy 1759 GGAACTTGGTTTATTCAAAAGTCAGGGCGTTAGAGATTACATGATAGAACTCCTAAT 1818
Db 564 GlyAspLeuIle-----AspPheIysAspHisPheIysIleThrCysGlnHisSerAsn 581
Qy 1819 TCTACACAATCTTATACATAGCTTCGATACGCTACAAATGGTGGCGGAAATCTCTT 1878
Db 582 PheGlnGlnSerTyPheIleargIleargTyAlaSerAsnGlySerAlaSerThrArg 601
Qy 1879 CCTAATATATCTTCAATACACAGAGTAATAGGAATACCACCTCAACGCTCAACAAAC 1938
Db 602 AlaValIleAsnLeuSerIleProGlyValAlaGluLeu--GlyMetAlaLeuAsnPro 620
Qy 1939 ACTTTTCTGGTACAAATTAATTAATTTACATACGAGATTTGGGTATTTCCAAATTT 1998
Db 621 ThrPheSerGlyThrAspTyThrAsnLeuIysTyIysAspPheGlnTyLeuGluPhe 640
Qy 1999 CCAAGTCAGTAACATTACCTTTAAATCGAAACATACCAATTATATTTAAATCGTCAGAT 2058
Db 641 SerAsnGluValIysPheAlaProAsnGlnAsnIleSerLeuValPheAsnArgSerAsp 660
Qy 2059 GTA---TCAAAATCAATTTAATCATGATGAAATGAAATTTATACCAATTTCTCTCT 2115
Db 661 ValTyThrAsnThrThrValLeuIleAspIysIleGluPheLeuProIleThrArgSer 680
Qy 2116 GTAGCCAAATAGAGAAACAAATAGAACTATCCAAACAAATTAATTAATTTATACATTT 2175
Db 681 IleArgGluAspArgGluIysGlnIysLeuGluThrValGlnGlnIleAsnThrPhe 700
Qy 2176 TTCACAAATCATACAAATAATCTTTAAATATAGAAAGCCACAACTATGATATTGAT 2232
Db 701 TyrAlaAsnProIleIysAsnThrLeuGlnSerGluLeuThrAspTyAspIleAsn 719

RESULT 3
B29838
parasporal crystal protein - Bacillus thuringiensis subsp. israelensis (fragment)
C:Species: Bacillus thuringiensis subsp. israelensis
C>Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 05-Oct-2004
C:Accession: B29838
R:Thorne, L.; Garduno, F.; Thompson, T.; Decker, D.; Zounes, M.; Wild, M.; Walfield, A.M.
J. Bacteriol. 166, 801-811, 1986
A:Title: Structural similarity between the Lepidoptera- and Diptera-specific insecticidal
A:Reference number: A94672; MUID:86223796; PMID:3011746
A:Accession: B29838
A:Molecule type: DNA
A:Residues: 1-934 <THO>
A:Cross-references: UNIPROT:P09662; UNIPARC:UPI00001781A0; GB:M12662; NID:g143228

Alignment Scores:
Pred. No.: 1,19e-52 Length: 934
Score: 923.50 Matches: 262
Percent Similarity: 47.26% Conservative: 117
Best Local Similarity: 32.67% Mismatches: 270
Query Match: 23.45% Indels: 153
DB: 2 Gaps: 34

US-10-782-570-1 (1-2235) x B29838 (1-934)
Qy 13 AATAAATGAATGATGAGATTATCGATTCAAGAAATTTATCTTATCTTCTTAACAGAAAT 72
Db 6 AsnIysAsnGluTyGluIlePheAsnAlaProSerAsnGlyPheSerLysSerAsnAsn 25
Qy 73 ATTGATCAATCTAGTACCTTACCAATTAATCCAAATCAACCAATTAACAAACACAAAT 132
Db 26 -----TyrSerArgTyProLeuAlaAsnIysProAsnGlnProLeuIysAsnThrAsn 43
Qy 133 TACAAGAGTGGCTCAATATGTGTCAAGGGAATACACAAATATGGTGATAATTCGAGACA 192
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Db 44 TyrIysAspTrpLeuAsnValCysGlnAspAsnGlnGlnIleTyThrGlyAsnAsnAlaGlyAsn 63
Qy 193 TTTGCTAGTGTGATACAAATTCGTCAGTGTAGTCAGGTACTATTGTATCGGTACTCTG 252
Db 64 PheAlaSerSerGluThrIleValGlyValSerAlaGlyIleIleValValGlyThrMet 83
Qy 253 TTAGCCCGTATAGTGGGCTCATTCTTATATCCGACCGATAGGAATAATATAGGTGCTATA 312
Db 84 LeuGly-----AlaPheAlaAlaPro-----ValLeuAlaAlaGly 95
Qy 313 ATAATATCTTTTGGTACCTTAATCAGCTGCTTTTGGCCCGCGGAGAACAGACAAACA 372
Db 96 IleIleSerPheGlnThrLeuLeuProIlePheTrp--GlnGlySerAspProAlaAsn 114
Qy 373 GTATGGACACAAATTTTAAATGGGAGAAATTTTGTGTATACACCGTCTTAACAGAA--- 429
Db 115 ValTrpGlnAspLeuLeuAsnIleGly-----GlyArgProIleGlnGluIle 130
Qy 430 -----AGCATAAACAGCTTAAGTTACAAACTTTAGAGGATTTAGACAAATATTACAA 483
Db 131 AspIysAsnIleIleAsnValLeuThrSerIleValThrProIleIysAsnGlnLeuAsp 150
Qy 484 AGCTATAATACAGCATTAGATGATTGGAGAAAATTAAAGAAAGACTACAAGCTCTGGATTA 543
Db 151 LysTyTrpGlnGluPhePheAspLysTrpGluProAlaArg----- 163
Qy 544 CCACCATCATCAGCATTTACCAACAGCTGCTTGAATCTTAAATAACGATTTGAGAATGTT 603
Db 164 -----ThrHisAlaAsnAlaIysAlaValHisAspLeuPheThrThrLeuGluProIle 181
Qy 604 CACAAAT-----GATTTTATTCGAGAAATACCTGTTTCCAACTTGAACCTTATAAA 654
Db 182 IleAspIysAspLeuAspMetLeuIysAsnAsnAlaSerTyArgIleProThr----- 199
Qy 655 ACGCTATTACTACTTATTATGCGAAGCTGCTAATTTTCATTTTAAATTTTATTATCAACAA 714
Db 200 -----LeuProAlaTyAlaGlnIleAlaThrTrpHisLeuAsnLeuLeuIysHis 216
Qy 715 GGTGCTGAATTTGGCTGATGAATGGATGCAGATATACATCTTCCAAATTTGAACCTAAT 774
Db 217 AlaAlaThrTyTrpIleTrp-----LeuGlnAsnGlnGlyIleAsnProSer 233
Qy 775 GCTGGAACATCAGATGATTTATAAA---CTTTTAAAGAAATATATACCTTAATATAGT 831
Db 234 ThrPheAsnSerSerAsnTyTrpGlnGlyTyLeuIysArgIysIleGlnGluTyThr 253
Qy 832 AACTATTGTGCAATACCTATAGAGAGGACTAAATAAATTCGAAACGAACTTAATATG 891
Db 254 AspTyTrpCysIleGlnThrTyAsnAlaGlyLeuThrMetIleArgThrAsnThrAsnAla 273
Qy 892 AGATGGAGTATATTAAATGATTCGAAAGATATATGACTATTAATCTGTTATGATGATATC 951
Db 274 ThrTrpAsnMetTyAsnThrTyArgLeuGluMetThrLeuThrValLeuAspLeuIle 293
Qy 952 GCTCAATTTCTTTTATGATATAAGAGATACAAAGATTCAAATGAGGAGATAGGTGGC 1011
Db 294 AlaIlePheProAsnTyAspProGluIysTyTrpProIle-----Gly 307
Qy 1012 ATTAAAACTGAACCTTACAGAGAAATTTATACAACTGAAATTAATTTTTCACCGCTTACT 1071
Db 308 VallysSerGluLeuIleArgGluValTy---ThrAsnValAsnSerAspThrPheArg 326
Qy 1072 TACCTTGAATTCACCCCAATCTCGCTAATATGAATATATTAATTAACACGTTTCAGGGCTT 1131
Db 327 -----ThrIleThrGluLeuGluAsnGlyLeuThrArgAsnPro--- 339
Qy 1132 AGATTATTTTCAATTTTAGATGAATTTATATTTTATATACAAATAT----- 1176
Db 340 ThrLeuPheThrTrpIleAsnGlnGlyArgPheTyThrArgAsnSerArgAspIleLeu 359
Qy 1177 GAAACGCTAC-----GGGAATCGTTTACGTGTTGTTATGTTATTCGAAATCGTAAT 1218
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Db 360 AspProTyrAspIlePheSerPheThrGlyAsnGlnMetAla----- 373
Qy 1219 AGATCTACTTATGCTACGACAGGAACTGAAATTTATATATGAGAAAGACAGGT----- 1272
Db 374 ---PheThrHisThrAsnAspAspArgAsnIleIleTrpGlyAlaValHisGlyAsnIle 392
Qy 1273 ---CCACCCACCAACAAACTTTTAAATCACTTTGAATCCTAT-----AAAGTT 1317
Db 393 IleSerGlnAspThrSerLysValPheProPheTyrArgAsnLysProIleAspLysVal 412
Qy 1318 TCAATTGTAAGTATGATGACAGTAAGTAAGTAACTCTACTCTCCCTTTTCCTAACATATATCTTTACA 1377
Db 413 GluIleValArgHisArgGlu-----TyrSerAsp 422
Qy 1378 ATTAATCAAAATGAACTTTTATTAATAATTCACCTAGTATATAATAATTAACATATATTCAGCT 1437
Db 423 IleIleTyrGluMetIlePhePheSerAsnSer---SerGluValPheArgTyrSerSer 441
Qy 1438 GGGGGGAATTTATCTTAATGATGATAAAACAACTGATTTTCAATTTCTCTGTTAAAAAAGAC 1497
Db 442 AsnSerThrIleGluAsnAsnTyrLysArgThrAspSerTyrMetIleProLysGlnThr 461
Qy 1498 TGTAACCAATTAATTAATCCAAATGTTTACCAAGCTATATAGTATATAGTATATTTA 1557
Db 462 TrpLys-----AsnGluGluTyrGlyHisThrLeu 471
Qy 1558 TCCAGTCTTTCTTTATTTATTTATTTCTTATAAATTTGATTTAGCTGCTAAATATATATAT 1617
Db 472 SerTyrIleLysThrAspAsnTyrIlePheSerVal-----ValArgGluArg 488
Qy 1618 ACAGTGCTATAGGATGACACACATAGTATGTTTATAGAAATATAGCAATATTCAGATATA 1677
Db 489 ArgValAlaPheSerTyrThrHisThrSerValAspPheGlnAsnThrIleAspLeuAsp 508
Qy 1678 ATAATTCAATGATCCCGCAATCAAGGTAACTGCTTGTATACAACTCTAAGTAAT 1737
Db 509 AsnIleThrGlnIleHisAlaLeuLysAlaLeuLysValSerSerAspSerLysIleVal 528
Qy 1738 GAAGGCTGCTCATACAGGAGAACTGCTTTATTTTCAAGTCAAGGCGGTTTAG 1797
Db 529 LysGlyProGlyHisThrGlyGlyAspLeuValIleLeuLysAspSer-----MetAsp 546
Qy 1798 ATTCATCATGAGA---ACTCCTAAATCTACACATCTTATTATACATAGACTCGACCT 1854
Db 547 PheArgValArgPheLeuLysAsnValSerArgGlnTyrGlnValArgIleArgTyrAla 566
Qy 1855 ACAATGCTGCTGGAATATCTCTCTTAATATATCTTACAAATACCAAGGAGTAAATAGGA 1914
Db 567 ThrAsnAla-----ProLysThrThrValPheLeuThrGlyIleAspThr 581
Qy 1915 ATACACCTCAACGACTCAACACACTTTTCTGTCACAAATTAAT-----AATTGA 1968
Db 582 IleSerValGlu---LeuProSerThrThrSerArgGlnAsnProAsnAlaThrAspLeu 600
Qy 1969 CAATACGAGAGATTTGGGTATTTCCAAATTTCCAAAGTACAGTA----- 2010
Db 601 ThrTyrAlaAspPheGlyTyrValThrPheProArgThrValProAsnLysThrPheGlu 620
Qy 2011 -----ACATTACCTTTAAATCGAAACATACCATTTATATTTAAATCGTCAGATGTA 2061
Db 621 GlyGluAspThrLeuLeuMetThr-----LeuTyrGlyThrProAsnHis 635
Qy 2062 TCAATTAATTTAATCATGATAAATTTGATTTATACCAATTTATCTCTCTCTGTCAGC 2121
Db 636 SerTyrAsnIle---TyrIleAspLysIleGluPheIleProIleThrGlnSerValLeu 654
Qy 2122 CAAATAGAGAAACAAATAATTTAGAACTATCCAA----- 2157
Db 655 AspTyrThrGluLysGlnAsnIleGluLysThrGlnLysIleValAsnAspLeuPheVal 674
Qy 2158 -----ACAAAAATA----- 2166
Db 675 AsnAsnLysValLeuThrIlysIleAspSerMetAlaValLysAlaArgLysValVal 694

Qy 2167 AATACATTTTTCACAAATCATACAAATACTTTTAAATATAGAACCCACAACTATGAT 2226
Db 695 AsnProMetPheThrSerGlyAlaLysAsnArgLeuLysLeuGluThrThrAspTyrGlu 714
Qy 2227 ATTGAT 2232
Db 715 IleAsp 716
RESULT 4
USBS91
paraesoparal crystal protein cry4Ba1 [validated] - Bacillus thuringiensis subsp. israeliensis
N;Alternate names: delta-endotoxin Bt6; insecticidal protein ISRH3; mosquitoicidal 130K p
C;Species: Bacillus thuringiensis subsp. israeliensis
C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text change 05-Oct-2004
C;Accession: S00398; A37587; J70315; A28541; I39869; I40584
R;Chungjatupornchai, W.; Hofste, H.; Seurinck, J.; Anguthanasombat, C.; Vaeck, M.
Eur. J. Biochem. 173, 9-16, 1988
A;Title: Common features of Bacillus thuringiensis toxins specific for Diptera and Lepid
A;Reference number: S00398; MUID:88185334; PMID:2833395
A;Accession: S00398
A;Molecule type: DNA
A;Residues: 1-1136 <CHU>
A;Cross-references: UNIPROT:P05519; UNIPARC:UPI0000001B1D; EMBL:X07423; NID:G40353; PIDN
R;Yanamoto, T.; Watkinson, I.A.; Kim, L.; Sage, M.V.; Stratton, R.; Akande, N.; Li, Y.;
Gene 66, 107-120, 1988
A;Title: Nucleotide sequence of the gene coding for a 130-kDa mosquitoicidal protein of B
A;Reference number: J70315; MUID:88329719; PMID:2901387
A;Accession: A37587
A;Molecule type: DNA
A;Residues: 1-13 <YA2>
A;Cross-references: UNIPARC:UPI00001747C0
A;Note: the majority of sequence differences are consistent with frameshift errors
R;Tungpradubkul, S.; Settassatien, C.; Panyim, S.
Nucleic Acids Res. 16, 1637-1639, 1988
A;Title: The complete nucleotide sequence of a 130 kDa mosquito-larvicidal delta-endotox
A;Reference number: A28541; MUID:88157738; PMID:2831510
A;Accession: A28541
A;Molecule type: DNA
A;Residues: 1-204, 'R', 206-1136 <TUN>
A;Cross-references: UNIPARC:UPI000016EA3C; EMBL:X07082; NID:G40309; PIDN:CAA30114.1; PID
R;Sen, K.; Honda, G.; Koyama, N.; Nishida, M.; Neki, A.; Sakai, H.; Himeno, M.; Komano,
Agric. Biol. Chem. 52, 873-878, 1988
A;Title: Cloning and nucleotide sequences of the two 130 kDa insecticidal protein genes
A;Reference number: I39869
A;Accession: I39869
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-202, 'C', 205-271, 'L', 273-324, 'Y', 326-1136 <RES>
A;Cross-references: UNIPARC:UPI0000156E4D; GB:D00247; NID:G216287; PIDN:BA00178.1; PID:
R;Anguthanasombat, C.; Chungjatupornchai, W.; Kertbundit, S.; Luxanani, P.; Settassat
Mol. Gen. Genet. 208, 384-389, 1987
A;Title: Cloning and expression of 130-kd mosquito-larvicidal delta-endotoxin gene of Ba
A;Reference number: I40584; MUID:88038331; PMID:2890080
A;Accession: I40584
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-142 <RE2>
A;Cross-references: UNIPARC:UPI000016EA41; EMBL:X05692; NID:G40350; PIDN:CAA29174.1; PID
C;Comment: This protein is toxic to many lepidopteran larvae.
C;Superfamily: Parasporal crystal protein
C;Keywords: delta-endotoxin
Alignment Scores: 7.61e-46 Length: 1136
Pred. No.: 819.00 Matches: 246
Score: 47.70% Conservative: 117
Percent Similarity: 32.33% Mismatches: 268
Best Local Similarity:


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Db 615 LeuAenMetThrSerAenAenGlnValIleIleAenArgIleGluIleIleProIleThr 634
Qy 2110 TCCTCTGACGCCAAATAGAGAAACACAAAATAGAAATATCCAAACAAAATAAT 2169
Db 635 GlnSerValLeuAenGluThrGlnAenGlnAenLeuGluSerGluArgGluValValAen 654
Qy 2170 ACATTTTTCACAAATACATACAAAATATCTTTAAATATAGAAGCCACAAATATGATATT 2229
Db 655 AlaLeuPheThrAenAenAlaLeuAenAlaLeuAenIleGlyThrThrAenPheAspIle 674
Qy 2230 GAT 2232
Db 675 Asp 675

RESULT 5
S10228
parasporeal crystal protein cry3Ba1 - Bacillus thuringiensis (fragment)
N:Alternate names: coleopteran-active parasporal crystal protein; delta-endotoxin
C:Species: Bacillus thuringiensis
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
C:Accession: S10228
R:Sick, A.; Gaertner, F.; Wong, A.
Nucleic Acids Res. 18, 1305, 1990
A>Title: Nucleotide sequence of a coleopteran-active toxin gene from a new isolate of Ba
A:Reference number: S10228; MUID:90206811; PMID:2320431
A:Accession: S10228
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-659 <SIC>
A:Cross-references: UNIPROT:P17969; UNIPARC:UP10000126C13; EMBL:X17123; NID:G40258; PIDN
C:Genetics:
A:Gene: cryIIIB
C:Superfamily: Parasporal crystal protein
C:Keywords: delta-endotoxin; toxin

Alignment Scores:
Pred. No.: 1,73e-38 Length: 659
Score: 706.00 Matches: 216
Percent Similarity: 44.27% Conservative: 116
Best Local Similarity: 28.80% Mismatches: 270
Query Match: 17.92% Indels: 148
DB: 2 Gaps: 31

US-10-782-570-1 (1-2235) x S10228 (1-659)
Qy 1 GTGAATCAAAATAAATAATGAATATGAGATATCGAT---TCAAGAATTTATCTTAT 57
Db 9 MetAenProAenAenAenArgSerGluThrAspThrIleLysValThrProAenSerGluLeu 28
Qy 58 CTTCTTAACAGAAATATGATCATCTAGATACCTTACACAAATATCCAAATCAACCA 117
Db 29 ProThrAen-----HisAenGlnThrProLeuAlaAenAenProAenSerThr 44
Qy 118 TTACAAACACAAATATCAAGAGGCGCTCAATATGTCGAAGGCAATACACAAATATGTT 177
Db 45 LeuGluGluLeuAenThrLysGluPheLeuArgMetThrAlaAenAenSerThr----- 62
Qy 178 GATAATTTTCGACACATTTGCTAGTCTGATACAAATTTGCTGCGAGTTAGTGCAGGTACTATT 237
Db 63 -----GluValLeuAenAenSerThrValLysAenAenAlaValGlyThrGlyIleSer 79
Qy 238 GTATCCGGTACTCTGTTAGCCGGTATAGTGGGCTCATTCTATATATCCGGACCGATAGGA 297
Db 80 ValValGlyGlnIleLeuGlyValValGly-----ValPro 91
Qy 298 ATAATAGGTGCTATATAATATCTTTTGTACCCCTAATCACTGTCTTTTGGCCCGCGGA 357
Db 92 PheAlaGlyAlaLeuThrSerPheThrGlnSerPheLeuAenAlaIleThrProSer--- 110
Qy 358 GAACAAAGACAAACAGTATGACACAAATTTTAAATATGGGAGAAATTTTGTGTGATACA 417
Db 111 -----AspAlaAenProThrLysAlaPheMetAlaGlnValGluValLeuIleAenLys 128
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Qy 418 CCGTTAACAGAAACATATAAACAGCTAAAGTTTACAACTTTAGAGGATTTAGACAAATA 477
Db 129 LysIleGluGluThrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAenAen 148
Qy 478 TTACAAAGCTATATATACAGCATTAGATGATGGAGAAAATTTAAAAGACTACAAGCTCCT 537
Db 149 PheGluAenPheValAenAlaLeuAenSerTrpLysLys----- 161
Qy 538 GGATTACACCATCATGACATTTACAAAGCTCCCTTGACTCTTAAATATAGATTGAG 597
Db 162 ---AlaProValAenLeuArgSerArgSerGlnAenAenArgIleArgGluLeuPheSer 180
Qy 598 AATGTTCAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTTGAACTTATAAAACG 657
Db 181 GlnAlaGluSerHisPheAenAenSerMetProSerPheAlaValSerLysPheGluVal 200
Qy 658 CTATTACTACTATTTATGCGCAAGCTGCTAAATTTTCAATTTAAATTTTATTAACAACAGGT 717
Db 201 LeuPheLeuProThrTyAlaGlnAlaAenThrHisLeuLeuLeuLeuLysAspAla 220
Qy 718 GCTGAATTTGGCTGATGAATGGAATGCAGATATACATCTCTCACAAATTTGAACCTAATGCT 777
Db 221 GlnValPheGlyGluGluTrpGlyTy----- 229
Qy 778 GGAACATCAGATGAC-----TATTATAAACTTTTAAAGAAATATACCTAAATAT 828
Db 230 ---SerSerGluAenPheIleAlaGluPheTyGlnArgGlnLeuLysLeuThrGlnGlnTy 248
Qy 829 AGTAACTATTGTGCAATATACCTATAGAGAGGACTAAATAAACTTCGAAACGAACTAAT 888
Db 249 ThrAspHisCysValAenAenTrpTyAsnValGlyLeuAenSerLeuAenGlySerThrTy 268
Qy 889 ATGAGATGGAGTATTTAATGATTCGAAGATATATGACTATATCTGTTATAGATACT 948
Db 269 AspAlaTrpValLysPheAenAenArgPheArgGluMetThrLeuThrValLeuAenLeu 288
Qy 949 ATCGCTCAATTTCTTTTATGATATAAGAGATACAAAGATTTCAATAGGAAGATAGT 1008
Db 289 IleValLeuPheProPheTyAspValArgLeuTySerLys----- 302
Qy 1009 GGCATTAAACTGAACTTTACAGAGAAATTTATACAACTGAAATATAATTTTGACGCTTT 1068
Db 303 GlyValLysThrGluLeuThrArgAspIlePheThrAspProIle---PheThrLeuAen 321
Qy 1069 ACTTACCTTGAAATTCACCCCAATCTCGCTATATATGATATATAATTTAACAGTTTCAGGG 1128
Db 322 AlaLeuGlnGluTyGlyProThrPheSerSerIleGluAenSerIleArgLysPro--- 340
Qy 1129 CTTAGATTTATTTTCAATTTTATAGATGAATCTTATATTTTATACAAA----- 1173
Db 341 ---HisLeuPheAenPheTyLeuArgGlyIleGluPheHisThrArgLeuArgProGlyTy 359
Qy 1174 -----AATGAAACGTPACGGGAATCGTTTGTGTTTGTGTTTTCGAAATCGT 1215
Db 360 SerGlyLysAenSerPheAenTyTrpSerGlyAenTy-----ValGluThrArg 376
Qy 1216 AATGATCTCTATGCTACGACGAACTGAAATATATATATATATGGAAGAAGACAGGTCCA 1275
Db 377 ProSerIleGlySerAenAenThrIleThrSerProPheTyGlyAspLysSerIleGlu 396
Qy 1276 CCCCAACAAACCTTTTAATACCATTTGAATCCTATAAGATTTCAATGTTAATGATGATAGA 1335
Db 397 ProIleGlnLys-----LeuSerPheAenGlyGlnLysValTy-----Arg 410
Qy 1336 CAAGTA-----ACTCTACTTCCCTTTTCCCTAAC-----ATATACTTTTCAATTAAT 1383
Db 411 ThrIleAlaAenThrAspIleAlaAlaPheProAenGlyLysIleTyPheGlyValThr 430
Qy 1384 CAATTTGAACCTTTATTTAAATTAATTCACCTAGTAAATTAATTA-----ACATATCA 1434
Db 431 LysValAenPheSerGlnTyAspAenGlnLysAenGluThrSerThrGlnThrTyAsp 450
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QY 1435 GCT-----CGGGGGAATTTATCTAATGATAAA-----AAA 1464
Db SerIysArgTyrAsnGlyTyrLeuGlyAlaGlnAspSerIleAspGlnLeuProGlu 470
QY 1465 ACAACCTGATTTTCAATTTCTGTAAATAAAGACTGTAAACCAATATTAAATCCAAATGTT 1524
Db ThrThrAsp-----GluProLeuGluLys----- 478
QY 1525 TTACCAAGCTATAATAGTTATAGTCATATTTATCCAGTGTTCCTTTATTAATTAATTC 1584
Db AlatySerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGln 493
QY 1585 TATAAATTTGGATTAGCGCTAAATATATATATACAGCTGCATAGGATGACACACAGT 1644
Db AspArgArgGlyThrIle-----ProPhePheThr-----TrpThrHisArg 507
QY 1645 AGTGTTAATAGAAAATAATGCAATATACAGATAAAATAATTAACAATGATCCAGCAATCAA 1704
Db SerValAspPhePheAsnThrIleAspAlaGluLysIleThrGlnLeuProValValLys 527
QY 1705 GGTAAACAGCTTTGATACAAACTCTTAAGTAATTAAGGACCTGTGTCATACAGGAGAAAC 1764
Db AlatyAlaLeuSerSerGlyAlaSerIleGluGlyProGlyPheThrGlyGlyAsn 547
QY 1765 TTGGTTTATTACAA-----AGTCNAGGCGCTTTAGAGATTACATGTAGAACT 1812
Db LeuLeuPheLeuLysGluSerSerAsnSerIleAlatyPheLeValThrLeuAsnSer 567
QY 1813 CCTAATCTCACACATCTTATACATAGACTTCGATACGCTACAAATGGTGTCTGGAAT 1872
Db AlaAlaLeuLeuGlnArgTyrArgValArgIleArgTyrAlaSerThr----- 583
QY 1873 ACTTCTCTATATATCTTTACAAATACAGGAGTAAATAGGAATACCACTCAACGACTC 1932
Db ThrAsnLeuArgLeuPheVal-----GlnAsnSer 593
QY 1933 AACACACTTTCTGGTACAAATATATATATATTTACAAATAC-----GGAGATTTTGGG 1986
Db AsnAsnAspPheLeuValIleTyrIleAsnLysThrMetAsnIleAspGlyAspLeuThr 613
QY 1987 TAT-----TTCCAAATTTCCAGTACGTAACATTTACCTTTTAAATTCGAAACATACCACTT 2040
Db TyrGlnThrPheAspPheAlaThrSer-----AsnSerAsnMetGlyPhe 628
QY 2041 ATATTAAATCGTCAGAT-----GTATCAAAATTCAAATTTA 2076
Db SerGlyAspThrAsnAspPheIleGlyAlaGluSerPheValSerAsnGluLysIle 648
QY 2077 ATCATTTGATAAAATTTGAATTTATACCAATT 2106
Db TyrIleAspLysIleGluPheIleProVal 658

RESULT 6
I39811
Parasporal crystal protein cry3Bb1 - Bacillus thuringiensis
N:Alternate names: parasporal crystal protein cryIIIB2
C:Species: Bacillus thuringiensis
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 05-Oct-2004
C:Accession: I39811
R:Donovan, W.P.; Rupar, M.J.; Slaney, A.C.; Malvar, T.; Gawron-Burks, M.C.; Johnson, T.E
Appl. Environ. Microbiol. 58: 3921-3927, 1992
A:Title: Characterization of two genes encoding Bacillus thuringiensis insecticidal crys
A:Reference number: I39811; MUID:93119147; PMID:1476436
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-652 <RES>
A:Cross-references: UNIPROT:Q06117; UNIPARC:UPI0000126C14; GB:M89794; NID:g142729; PIDN:
C:Gene: cryIIIB2
C:Superfamily: Parasporal crystal protein
Alignment Scores:

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Pred. No.: 1.64e-37 Length: 652
Score: 691.00 Matches: 208
Percent Similarity: 44.84% Conservative: 122
Best Local Similarity: 28.26% Mismatches: 286
Query Match: 17.54% Indels: 120
DB: 2 Gaps: 28

US-10-782-570-1 (1-2235) x I39811 (1-652)

QY 1 GTGAATCAAAATATAAATGAATATGAGATTATCGATTCAAGAATTTTATCTTATCCT 60
Db MetAsnProAsnAsnArgSerGluHisAspThrIle-----LysValThrProAsn 17
QY 61 TCTAACAGAAATATTGATCTATTAGTACCTTACACAAATATATCAAAATCAACCATTA 120
Db SerGluLeuGlnThrAsnHisAsnGlnTyrProLeuAlaAspAsnProAsnSerThrLeu 37
QY 121 CMAAACACAAATTACAAAGAGTGGCTCAATATGTGTCAA---GGGAATACACAATATGGT 177
Db GluGluLeuAsnTyrIysGluPheLeuArgMetThrGluAspSerThrGluValLeu 57
QY 178 GATAAATTTTCGAGACATTTGCTAGTGTGATACAAATTTGCT---GCAGTTAGTCAGGACT 234
Db AspAsn-----SerThrValLysAspAlaValGlyThrGlyIle 70
QY 235 ATTGTATCCGGTACTCTGTAGCGGTATAGTGGGCTCACTTCTATATCCGGACCGATA 294
Db SerValValGlyGlnIleLeuGlyValValGly-----Val 82
QY 295 GGAATAATAGTGTCTAATAAATATCTTTTGGTACCCTAATCTACTGTCTTTTGGCCGCG 354
Db ProPheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnThrIleTrpProSer 102
QY 355 GGAGAACACAGACAAAACAGTATGACACAAATTTATTAAAAATGGAGAAATTTTGTTCAT 414
Db AspAlaAspProTrpLysAlaPheMetAlaGlnValGluValLeuLeuAsp 119
QY 415 ACACCGTTACAGAAACATATAACAGCTAAAGTTACAAACTTTAGAGAGATTAGACAA 474
Db LysLysIleGluGluTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAsn 139
QY 475 ATATTACAAAGCTATAATACAGATTTAGATGATGGAGAAATTTAAAAAGACTACAAGCT 534
Db AsnPheGluAspTyrValAsnAlaLeuAsnSerTrpLys----- 153
QY 535 CTGGATTACCACTCATCAGCATTTACAAACAGCTCGCTTGACTCTTAAATACGATTT 594
Db ThrProLeuSerLeuArgSerLysArgSerGlnAspArgIleArgGluLeuPhe 171
QY 595 GAGAAATGTTCAATGATTTTATTCGAGAAATACCTGGTTTCCACTTGAACCTTATAA 654
Db SerGlnAlaGluSerHisPheArgAsnSerMetProSerPheAlaValSerLysPheGlu 191
QY 655 ACCTATTACTACTATTTATGCGAAGCTGCTAAATTTTCATTTAAATTTTATTACACAA 714
Db ValLeuPheLeuProThrTyrAlaGlnAlaAsnThrHisLeuLeuLeuLeuLeuAsp 211
QY 715 GGTGCTGAATTTGGCTGATGAATGGAATGACAGATATACATCTCTTCCAAAATTTGAACCTAAT 774
Db AlaGlnValPheGlyGluGluTrpGlyTyrSer-----Ser 223
QY 775 GCTGGAACATCAGATGACTATTATAAATCTTTTAAAGAAATATATACCTAAATATAGTAAC 834
Db GluAspValAlaGluPheTyrHisArgGlnLeuLysLeuThr---GlnGlnTyrThrAsp 242
QY 835 TATTGTCRAATACCTATACAGAGAGCTAAATAAATCTCGAAACGAACCTAATATATGAGA 894
Db HisCysValAsnTrpTyrAsnValGlyLeuAsnGlyLeuArgGlySerThrTyrAspAla 262
QY 895 TGGAGTATATTAAATGATTATCGAAGATATATGACTATTACTGTATTAGTACTATCGCT 954
Db TrpValLysPheAsnArgPheArgGluMetThrLeuThrValLeuAspLeuIleVal 282

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Qy	955	CAATTTCTTTTATGATATATAAGAGANATCAAGATTCAATAGCAAGATAGTGGCAT	1011
Db	283	LeuProPheTyrAspIleArgLeuTyrSerLys-----GlyVal	296
Qy	1015	AAAACTGAACCTTACAGAGAAATTTATACAACTGAAATAAATTTGACCGTCTTACTTAC	1074
Db	297	LysThrGlnLeuThrArgAspIlePheThrAspProIle---PheSerLeuAsnThrLeu	315
Qy	1075	CTTGAAATTCACCCCAATCTCGCTATATAATGGAATATAAATTAACAGCTTCAGGCTTAGA	1134
Db	316	GlnGluTyrGlyProThrPheLeuSerIleGluAsnSerIleArgLysPro-----His	333
Qy	1135	TTATTTTCATTTTATAGTAGAATCTATATTTTATACAAA-----	1173
Db	334	LeuPheAspTyrLeuGlnGlyIleGluPheHisThrArgLeuGlnProGlyTyrPheGly	353
Qy	1174	-----AATGAAACGTACGGGAATCGTTTAGTTGGTATTCGAATCGTAATAGA	1221
Db	354	LysAspSerPheAsnTyrTrpSerGlyAsnTyr-----ValGluThrArgProSer	370
Qy	1222	TCTACTTATCTACGACGGAACCTGAAATATATATGAGAGAAACAGGTCACCACCACA	1281
Db	371	IleGlySerSerLysThrIleThrSerProPheTyrGlyAspLysSerThrGluProVal	390
Qy	1282	ACAAAACTTTAATACCATTTGAATCTCTAATAAGTTTCAATGTAACTGATGACAGAATG	1341
Db	391	GlnLys-----LeuSerPheAspGlyGlnLysValTyr-----ArgThrIle	404
Qy	1342	-----ACTCTACTCCCTTTTCTTAAC-----ATATACTTTCAATTAATCAATTT	1389
Db	405	AlaAsnThrAspValAlaIleTrpAsnGlnLysValTyrLeuGlyValThrLysVal	424
Qy	1390	GAACCTTTATTAATAATTCACCTAGTAAATAAATA-----ACATATTCAGCT---	1437
Db	425	AspPheSerGlnTyrAspAspGlnLysAsnGluThrSerThrGlnThrTyrAspSerLys	444
Qy	1438	-----GGGGGGAATTTATCTAATGATAAAAAACAACCTGATTTTCAATTTCTGTAA	1491
Db	445	ArgAsnAsnGlyHisValSerAlaGlnAspSerIleAsp-----GlnLeuProProGlu	462
Qy	1492	AAAGACTGTAAACCAATTTATTCCAAATTTGTTTACCAGCTATATAGTTATAGTCAT	1551
Db	463	ThrThrAspGluProLeu-----GluLysAlaTyrSerHis	474
Qy	1552	ATTTTATCCCGAGTTTCTTTTATTAATTAATTCCTATAAAATGCGTAGCGCTAAATATA	1611
Db	475	GlnLeuAsnTyrAlaGluCysPheLeuMetGlnAspArgGlyThrIle-----Pro	492
Qy	1612	TTATATACAGGTGCATTTAGGATGGACACACAGTAGTGTGTTAATAGAATAATGCAATATCA	1671
Db	493	PhePheThr-----TrpThrHisArgSerValAspPhePheAsnThrIleAsp	508
Qy	1672	GATAAATATATTACAATGATCCCGACCAATCAAGGTAAACAGCTTTGATACAACACTTAAG	1731
Db	509	AlaGluLysIleThrGlnLeuProValValLysAlaTyrAlaLeuSerSerGlyAlaSer	528
Qy	1732	GTAATTCGAAGCACTGTGTCATACAGGAGGAAACTTGGTTTATTTACAA-----	1779
Db	529	IleIleGluGlyProGlyPheThrGlyGlyAsnLeuLeuPheLeuLysGluSerAsn	548
Qy	1780	AGTCNAGGGCGCTTTAGAGATTTACATGTAGAACCTCTCAATTTCTACACAATCTTATTA	1839
Db	549	SerIleAlaLysPheLysValThrLeuAsnSerAlaAlaLeuLeuGlnArgTyrArgVal	568
Qy	1840	AGACTTCGATACGCTACAAATGGTGGGAAATTAATCTCTTCTATATATATCTCTTACA	1899
Db	569	ArgIleArgTyrAlaSerThr-----ThrAsnLeuArgLeuPheVal	582
Qy	1900	CCAGGAGTAAATAGGAATACCACTTCAACGACTCAACACCACTTTTCTGGTACAAATTA	1959
Db	583	-----GlnAsnSerAsnAsnAspPheLeuValIleTyrIle	594
Qy	1960	AAT-----AATTTACAAATACGAGATTTTGGTATTTTCCAAATTT	1998

Db 595 AsnLysThrMetAsnLysAspAspLeuThrGlnThrPheAspLeuAlaThrThr 614
 Qy 1999 CCAAGTACAGTAACATTACCTTTAAATCGAAACATACCACTTATATTAATTAATCGTCAGAT 2058
 Db 615 AsnSerAsnMetGlyPheSerGlyAspLysAsnGluLeuLeileGlyAlaGluSerPhe 634
 Qy 2059 GTATCAAAATTCAAATTTTAATCATGTATATAAAATGAAATTTATACAAAT 2106
 Db 635 ValSerAsnGluLysIleTyrIleAspLysIleGluPheIleProVal 650
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 A48944
 paraeoporal crystal protein cry7Aa1 - Bacillus thuringiensis
 N:Alternate names: paraeoporal crystal protein cryIIIC
 C:Species: Bacillus thuringiensis
 C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
 C:Accession: A48944
 R:Lambert, B.; Hottel, H.; Amys, K.; Jansens, S.; Soetaert, P.; Peferoen, M.
 Appl. Environ. Microbiol. 58, 2536-2542, 1992
 A:Title: Novel Bacillus thuringiensis insecticidal crystal protein with a silen
 A:Reference number: A48944; MUID:92384571; PMID:1514800
 A:Contents: BtS137J
 A:Accession: A48944
 A:Status: preliminary
 A:Molecule type: DNA; protein
 A:Residues: 1-1138 <LAW>
 A:Cross-references: UNIPROT:Q03749; UNIPARC:UPI000002C1E6; GB:M64478; NID:Q1427
 A:Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBIPI:112093)
 C:Superfamily: Paraeoporal crystal protein
 C:Keywords: delta-endotoxin
 Alignment Scores:
 Pred. No.: 2,59e-37 Length: 1138
 Score: 688.00 Matches: 220
 Percent Similarity: 44.50% Conservative: 128
 Best Local Similarity: 28.13% Mismatches: 288
 Query Match: 17.47% Indels: 146
 DB: 2 Gaps: 33
 US-10-782-570-1 (1-2235) x A48944 (1-1138)
 Qy 1 GTGAATCAAATAATAATAATGAATATGAGATTAATCGATTCAAAGAATTTATCTTATCCT 60
 Db 1 MetAsnLeuAsnAsnLeuAspGlyTyrGlu-----Asp 11
 Qy 61 TCTAACAGAAATATTGATCATCTCT--AGATACCCCTTACACAATAATCCAAATCAACCA 117
 Db 12 SerAsnArgThrLeuAsnAsnSerLeuAsnTyrProThrGlnLysAlaLeuSerProSer 31
 Qy 118 TTCAAAACACAAATTAACAAAGAGTGCTCAATATGTCTCAAGGGAATACACAATATGGT 177
 Db 32 LeuLysAsnMetAsnTyrGlnAspPheLysSerIleThrGlu-----Arg 46
 Qy 178 GATAATTTTCGAGACATTTGCTAGTCGTGAATACAATGCTGCGAGTTAGTCGAGGTACTATT 237
 Db 47 GluGlnProGluAlaLeuAlaSerGlyAsnThr-----AlaIleAsnThrValValSer 64
 Qy 238 GTATCCGGTACTCTGTTAGCCGGTATAGTGGGCTCACTCTATATCCGGACCGATGAG 297
 Db 65 ValThrGlyAlaThrLeuSerAla-----LeuGly 74
 Qy 298 ATAATAGTGTGTATAATAATATCT-----TTTGGTACCCCTTAATCACTGTCTTTTGGCCC 351
 Db 75 ValProGlyAlaSerPheIleThrAsnPheTyrLeuLysIleAlaGlyLeuLeuTyrPro 94
 Qy 352 CGCGGAGAACAGAACAAACAGTATGACACAAATTTATTAATATGGGAGAAATTTTGT 411
 Db 95 -----GluAsnGlyLysIleTyrAspGluPheMetThrGluValGluAlaLeuIle 111
 Qy 412 GATACACGTTTACAGAAAGACGATTAACAGCTAAAGTTTACAACTTTAGAGGATTTAGA 471
 Db 112 AspGlnLysIleGluGluTyrValArgAsnLysAlaIleAlaGluLeuAspGlyLeuGly 131

Qy	472	CAAAATATPACAAAGCTATAATAACAGCATTTAGATGATTTGGAGAAATATAAAAGACTCAA	531
Db	132	SerAlaLeuAepLysTyrrGlnLysAlaLeuAlaAepTrp-----LeuGlyLysGlnAep	149
Qy	532	GCTCCTGGATTACCAACCATCATCAGCATTACACAGCTGCCTGACTCTTAAATATACGA	591
Db	150	AspPro-----GluAlaLeuSerValAlaThrGlu	160
Qy	592	TTTCGAGAATGTTCAACATGATTTTATTCGAGAAATACCTGTTTCCAACTTGAACACTTAT	651
Db	161	PheArglleleAepSerLeuPheGluPheSerMetProSerPheLysValThrGlyTyrr	180
Qy	652	AAAACGCTATTACTACCTATTATATGCGCAAGCTCTCTAATTTCTCAATTTAAATTTATCAA	711
Db	181	GluIleProLeuLeuThrValTyrrAlaGlnAlaAlaAenLeuHisLeuAlaLeuLeuArg	200
Qy	712	CAAGCTGCTGAATTTGGCTGATGAATGGAATGCAGATATACATCTTCCAAATTTGAACCT	771
Db	201	AspSerThrLeuTyrrGlyAspLysTrpGly-----PheThrGlnAenAsnIleGluGlu	218
Qy	772	AATGCTGGAACATCAGATGACTATTATATAAATCTTTTAAAGAAATATATACCTAAATATAGT	831
Db	219	Asn-----TyrrAsnArgGlnLysLysArgIleSerGluTyrrSer	231
Qy	832	AACTATTGTGCAAAATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAACTAAATATG	891
Db	232	AspHisCythrLysTyrrTyrrAsnSerGlyLeuSerArgLeuAenGlySerThrTyrrGlu	251
Qy	892	AGATGGAGTATATTTAATGATATTCGAAGATATATGACTATTAATCTGATTAGATATCATC	951
Db	252	GlnTrpIleAenTyrrAsnArgPheArgGluMetIleLeuMetalAlaLeuAepLeuVal	271
Qy	952	GCTCAATTTCTTTTATGATATAAAGAGATACAAAGATTCATCAATAGGAGATAGGTGGC	1011
Db	272	AlaValPheProPheHisAepProArgArgTyrrSerMetGlu-----	285
Qy	1012	ATTAATAACTGAACTTACAAGAGAAATTTATACAACTGAAATATAATTTTGACCGCTTCTAT	1071
Db	286	ThrSerThrGlnLeuThrArgGluValTyrrThrAspProValSerLeuSer---IleSer	304
Qy	1072	TACCTGAAATTCACCAATCTCGCTATATATGGAATATATATTTAAACAGCTTCAGGCGCT	1131
Db	305	AsnProAspIleGlyProSerPheSerGlnMetGluAenThrAlaIleAenTyrrPro---	323
Qy	1132	AGATTATTTTCATTTTATGATGAACTTATATTTTATACA---AAAAATGAACGTACGGG	1188
Db	324	HisLeuValAspTyrrLeuAepGluLeuTyrrIleTyrrSerLysTyrrLysAlaPheSer	343
Qy	1189	AATCGTTTAT-----GTTGTTATTTGCAATCGT	1215
Db	344	HisGluIleGlnProAspLeuPheTyrrTrpSerAlaHisLysValSerPheLysLysSer	363
Qy	1216	AATAGATCTACTTATGCTACGACAGGAACGTGAATTTATATATATGAGAGAAACAGAGTCCA	1275
Db	364	GluGlnSerAenLeuTyrrThrGly-----IleTyrrGlyLysThrSerGly---	379
Qy	1276	CCCACACAAAACCTTTAATACCATTTGAATCTCTATAAGTTTCAATTTGAACCTGATAGA	1335
Db	380	-----TyrrIleSerSerGlyAlaTyrrSerPheHis---GlyAsnAspIle	393
Qy	1336	CAAGTAACCTCTACTTCCCTCTCTTCTTAAACATATAC-----TTTACAATT	1380
Db	394	TyrrArgThrLeuAlaAlaProSerValValValTyrrProTyrrThrGlnAenTyrrGlyVal	413
Qy	1381	AATCAAAATGAACTTTAT-----TTAAATTAATTCACCTAGTAATAAAA---	1422
Db	414	GluGlnValGluPheTyrrGlyValLysGlyHisValHisTyrrArgGlyLysAsnLysTyrr	433
Qy	1423	---TTACATATATTCAGCTGGGGGAATTTATCTAATCATGATATAAAAAACACTGATTTTCAA	1479
Db	434	AspLeuThrTyrrAspSerIleAspGlnLeuProAspGlyGlu-----	448

QY	1480	TTTCCTGTAAAAAAGACTGTAAACCAATATTATTAAATCCAAATTGTTTACCAAGCTATAAT	1539
DB	449	-----	452
QY	1540	AGTTATAGTCATATTTTATCCAG---TTTCTTTTATTTAATTATTCCTATAAAATTGGA	1596
DB	453	:	472
QY	1597	TTACGCGTAAATATATTATATACAGGTGCATTAGGATGGACACACAGTAGTGTGTTAATAGA	1656
DB	473	AsnAlaThrIleProIlePheSer-----TrpThrHisArgSerAlaGluTyr	488
QY	1657	AATATGCATATCAGATAAAATAATTACATGATCCAGCAATCAAAGTAACAGTCTT	1716
DB	489	TyrAsnArgIleTyrProAsnLysIleThrLysIleProAlaValLysMetTyrLysLeu	508
QY	1717	GATCAAACTCTAAGGTAAATTGAAGGACCTGGTCATACAGGAGGAACTGGTTTATTTA	1776
DB	509	AspAspProSerThrValValLysGlyProGlyPheThrGlyAspLeuValLysArg	528
QY	1777	CAAAAGTCARGGCGGTTTACAGATTTACATGTAGAACCTCTAATTCT-----ACACAATCT	1830
DB	529	GlySerThrGlyTyrIleGlyAspIleLysAlaThrValAsnSerProLeuSerGlnLys	548
QY	1831	TATTACATTAGACTTCGATACCGTACAAATGGTGCTGA-----AATACTCTTCCTAAT	1884
DB	549	TyrArgValArgValArgTyrAlaThrAsnValSerGlyGlnPheAsnValTyrIleAsn	568
QY	1885	ATATCTCTTCAATATACCAGGAGTAATAGGAATACCACCTCAAGGACTCAACACACTTTT	1944
DB	569	AspLysIleThr-----LeuGlnThrLysPhe	577
QY	1945	TCGTGGTACA-----AATTATAATAATTACAAATACGGAGAGATTTGGGTAT	1989
DB	578	GlnAsnThrValGluThrIleGlyGluGlyLysAspLeuThrTyrGlySerPheGlyTyr	597
QY	1990	TTCCAAATTTCCAGTACAGTAACATTACCTTTTAAATCGAAACATACCATTTATTTAAT	2049
DB	598	IleGluTyrSerThrThrIleGlnPhePro---AspGluHisProLysIleThrLeuHis	616
QY	2050	CGTGCAGATGTATCA---AATTCAAATTTTAAATCATTTGATAAAATTTGAATTTATACCAATT	2106
DB	617	LeuSerAspLeuSerAsnAsnSerPheTyr-ValAspSerIleGluPheIleProVal	636
QY	2107	ACTTCTCTGTACGCCAAATATAGAGAAAAACAAAATATAGAAACTATCCGAAACAAAAATA	2166
DB	637	AspValAsnTyr-----AlaGluLysGluLysLeuGluLysAlaGlnLysAlaVal	653
QY	2167	AATACATTTTTCACAAATCATACAAAAATACTTTAAATATAGAAGCCACCAACTATGAT	2226
DB	654	AsnThrLeuPheThr---GluGlyArgAsnAlaLeuGlnLysAspValThrAspTyrLys	672
QY	2227	ATTGAT	2232
DB	673	ValAsp	674

RESULT 8

paraesporal crystal protein cry8Ca1 - *Bacillus thuringiensis*
 N:Alternate names: paraesporal crystal protein cryIII
 C:Species: *Bacillus thuringiensis*
 C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Oct-2004
 C:Accession: I40589
 R:Sato, R.; Takeuchi, K.; Ogiwara, K.; Minami, M.; Kaji, Y.; Suzuki, N.; Hori, H.; Asano, S.
 Curr. Microbiol. 28, 15-19, 1994
 A:Title: Cloning, heterologous expression, and localization of a novel crystal protein g
 A:Reference number: I40589; PMID:94100786; PMID:7764305
 A:Accession: I40589
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-160 <RES>
 A:Cross-references: UNIPROT:Q45706; UNIPARC:UPI0000126CFE; EMBL:U04366; NID:G532523; PID:
 C:Superfamily: Paraesporal crystal protein

C;Keywords: delta-endotoxin

Alignment Scores: 2.85e-36 Length: 1160
 Pred. No.: 672.00 Matches: 216
 Score: 43.24% Conservative: 123
 Percent Similarity: 43.24% Mismatches: 317
 Best Local Similarity: 27.55% Indels: 128
 Query Match: 17.06% Gaps: 29
 DB:

US-10-782-570-1 (1-2235) x I40589 (1-1160)

QY 1 GTGAATCAAAATAATAAATAATGAAATATGAGATTATCGATTCAAGAAATTTATCTTATCCT 60
 DB 1 MetSerProAsnAsnGlnAsnGluTyrgluileileaspAlaLeuSerProThrSerVal 20
 QY 61 TCTAACAGAAATATTGATCATTTCTAGATACCTTTACACAAATATCCAAATCAACCATTA 120
 DB 21 SerAspAsnSerIle-----ArgTyrProLeuAlaAsnAspGlnThrAsnThrLeu 37
 QY 121 CAAAACACAAATATCAAAAGTGGCTCAATATGTGTCAAGG---AATACACAAATATGGT 177
 DB 38 GlnAsnMetAsnTyrLysAspTyrLeuLysMetThrGluSerThrAsnAlaGluLeuSer 57
 QY 178 GATAATTTTCGAGACATTTGCTAGTGTCTGATACAAATGTCTGAGTTAGTGCAGGTACTATT 237
 DB 58 ArgAsnProGlyThrPheIleSerAlaGlnAsp-----AlaValGlyThrGlyIleasp 75
 QY 238 GTATCCGGTACTCTGTAGCCGGTATAGTGGGCTCACTTCTATATCCGACCGCATGGA 297
 DB 76 IleValSerThrIleIleSerGlyLeuGly-----IlePro 87
 QY 298 ATAATAGTGTATATAATATCTTTGGTACCTCAATCACTGTCTTTGGCCCGCGGA 357
 DB 88 ValLeuGlyGluValPheSerIleLeuGlySerLeuIleGlyLeuLeuTyrProSerAsn 107
 QY 358 GAACAGCAAAACAGTAGTACACAAATTTATAAATGGGAGAAATTTTGTGTGATACA 417
 DB 108 AsnGluAsn-----ValTyrGlnIlePheMetAsnArgValGluGluLeuIleaspGln 125
 QY 418 CCGTTAACAGAAAGCAATAAAGCTAAAGTTTACAACTTTAGAGAGGATTTAGACAAATA 477
 DB 126 LysIleLeuAspSerValArgSerArgAlaIleAlaAspLeuAlaAsnSerArgIleAla 145
 QY 478 TTACAAAGCTATATACAGCATAGATGATGGAGAAATTTAAAGACTACAGCTCCT 537
 DB 146 ValGluTyrTyrGlnAsnAlaLeuGluAspTyrArgLys----- 158
 QY 538 GGATACCAACATCATCAGCATTAACAAGCTGCTTGTACTCTTTAAATACGATTTGAG 597
 DB 159 -----AsnProHisSerThr-----ArgSerAlaAlaLeuValLysGluArgPheGly 174
 QY 598 AATGTTCAATGATTTTATTCGAGAAATACCTGGTTTCCAACCTTGAACCTTATAAACG 657
 DB 175 AsnAlaGluAlaIleLeuArgThrAsnMetGlySerPheSerGlnThrAsnTyrGluThr 194
 QY 658 CTATTACTACCTATTATTCGCAAGCTGCTAATTTTCAATTTAATTTATTTACACAGGT 717
 DB 195 ProLeuLeuProThrTyrAlaGlnAlaAlaSerLeuHisLeuLeuValMetArgAspVal 214
 QY 718 GCTGAATTTGGCTGATGGAATGCAGATATACATCTTCCAAATTTGAACCTAATGCT 777
 DB 215 GlnIleTyrGlyLeuGluTyrGly-----TyrProGln----- 225
 QY 778 GGAACATCAGATGACTATTATAAACTTTTAAAGAAATATATACCTTAAATATAGTAACAT 837
 DB 226 AsnAspIleAspLeuPheTyrLysGluGlnValSerTyrThrAlaArgTyrSerAspHis 245
 QY 838 TTGCAATAACCTATAGAGAGAGACTAATAAATCTTCGAAACGAACCTAATATGAGATGG 897
 DB 246 CysValGlnTyrTyrAsnAlaGlyLeuAsnLysLeuArgGlyThrGlyAlaLysGlnTyr 265
 QY 898 AGTATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGATATCTGCTCAA 957

DB 266 ValAspTyrAsnArgPheArgArgGluMetAsnValMetValLeuAspLeuValAlaLeu 285
 QY 958 TTTTCTTTTATGATATAAGAGATACAAAGATTCAATAGGAAGAAATAGTGGCATTTAA 1017
 DB 286 PheProAsnTyrAsp-----AlaArgIleTyrProLeuGln 297
 QY 1018 ACT-----GAACCTTACAGAGAAATTTATACAACTGAAATATAAATTTTGACCGTCTTACT 1071
 DB 298 ThrAsnAlaGluLeuThrArgGluIlePheThrAspProValGly-----Ser 313
 QY 1072 TACCTTGAATTTCAACCAATCTCGCTATATATGGAATATATATTTTAACACGTTTCAGGCTT 1131
 DB 314 TyrValThrGlyGlnSerSerThrLeuIleSerTyrAspMetIleProAlaAlaLeu 333
 QY 1132 AGATTATTTTCAATTTTAGATGAATTTATA-----TTTATACAAAAATGAA 1179
 DB 334 ProSerPheSerThrLeuGluAsnLeuArgLysProAspPhePheThrLeuLeuGln 353
 QY 1180 ACGTACGGGAATCGTTTGTATTGGTATTCGGAATCGTAATAGATCTACTTATGTCTACGACA 1239
 DB 354 GluIle-----ArgMetTyrThrSerPheArgGlnAsn 364
 QY 1240 GGAACTGAAATTTATATATGGAAGAAAGACAGGTCCACCACACAAAAACTTTTAATA--- 1296
 DB 365 GlyThrIleGluTyrTyrAsnTyr-TripGlyGlnArgLeuThrLeuSerTyrIleTyr 384
 QY 1297 -----CAATTGAACTCTATATAAGTTTCAATTTGTAAGTGTAGTACAGTAAGTCTTACT 1350
 DB 385 GlySerSerPheAsnLysTyrSerGlyValLeuAlaGlyAlaGluAspIleProVal 404
 QY 1351 TCCCT-----TTCTCAACATATATAC 1371
 DB 405 GlyGlnAsnAspIleTyrArgValValTyrThrTyrIleGlyArgTyrThrAsnSerLeu 424
 QY 1372 TTTCAATTAATCAATTTGAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1431
 DB 425 LeuGlyValAsnProValThrPheTyrPheSerAsn-----AsnThrGlnLysThrTyr 442
 QY 1432 TCAGCTGGGGGAATTTATCTAATGATATAAATAAACAACACTGATTTTCAATTTCTCTGTAATA 1491
 DB 443 SerLysProLysGlnPheAlaGlyGlyIleLysThrIleAspSerGlyGluLeuThr 462
 QY 1492 AAAGACTGTAAACCAATTTATTAATCCAAATTTGTTTACCAGCTATAATAGTTATAGTCAAT 1551
 DB 463 TyrGlu-----AsnTyrGlnSerTyrSerHis 471
 QY 1552 ATTTTATCCCAAGTTTCTTTTATTTAATTTATTTTCTTATAAATTTGGATTAGCGCTAATATA 1611
 DB 472 ArgValSerTyrIleThrSerPheGluIleLysSerThrGlyGlyThrValLeuGlyVal 491
 QY 1612 TTATATACAGTGCTATGAGTACACACAGTGTAGTGTATAGTAATTAATGCAATATCA 1671
 DB 492 Val-----ProIlePheGlyTyrThrHisSerSerAlaSerArgAsnAsnPheIleTyr 509
 QY 1672 GATAAATAATTAACATGATCCCAAGCAATCAAGTAAAGTAACTCTTGATACAACTCTAAG 1731
 DB 510 AlaThrLysIleSerGlnIleProLeuAsnLysAlaSerArg-----ThrSerGlyGly 527
 QY 1732 GTAATTT-----GAAGGAGCTGGTGTACAGGAGGAGAACTGGTTTATTATACAA 1779
 DB 528 AlaValTyrAsnPheGlnGluGlyLeu-----TyrAsnGlyGlyProValMetLysLeuSer 546
 QY 1780 AGTCAGGG-----CGTTTAGAGATTATCATGATAGTACCTCTTAATTTCTACACA 1827
 DB 547 GlySerGlySerGlnValIleAsnLeuArgValAlaThrAspAlaLysGlyAlaSerGln 566
 QY 1828 TCTTATTATCATTAGACTTTCGATACGATCAATAGTGTCTGGAAT---ACTCTTCTCTAAT 1884
 DB 567 ArgTyrArgIleArgIleArgTyrAlaSerAspArgAlaGlyLysPheThrIleSerSer 586
 QY 1885 ATATCTCTTACATACACAGGAGTAAATAGGAATACCACTCAACGCTCAAC-----AAC 1938
 DB 1938


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Db      548 CysThrGluAsnGlySerAlaAlaThrIleTyrValThrProAspValSerTyrSerGln 567
      |||||
Qy      1828 TCTATTACATAGACTTCGATACCGTACAAATGGTGTGGAAATCTCTTCCTAAATATA 1887
      |||||
Db      568 LysTyrArgAlaArgIleHisTyrAlaSerThrSer-----GlnIle 581
      |||||
Qy      1888 TCTCTTAACAATACAGGAGTAAATAGAAATACCACTCAACGACTCAACACACACTTTTCT 1947
      |||||
Db      582 ThrPheThrLeu-----SerLeuAspGlyAlaPro-----PheAsnGlnTyrTyrPhe 597
      |||||
Qy      1948 GGTCAAAATATAAT-----AATTACAAATACGAGAGATTTTGGGTATTTCCAAATTT 1998
      |||||
Db      598 AspLysThrIleAsnLysGlyAspThrLeuThrTyrAsnSerPheAsnLeuAlaSerPhe 617
      |||||
Qy      1999 CCAAGTACAGTAACATTAACCTTTAAATCGAAACATACCATTTATATTAAATCGTGCAGAT 2058
      |||||
Db      618 SerThrProPheGluLeuSerGlyAsn---AsnLeuGlnIleGlyValThrGlyLeuSer 636
      |||||
Qy      2059 GTATCAAAATTCAAATTAATCAATTCATAAAATTTGAATTTATACCAATTT 2106
      |||||
Db      637 AlaGlyAspLysVal---TyrIleAspLysIleGluPheIleProVal 651

RESULT 11
S00873
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis
N:Alternate names: parasporal crystal protein cryA4
C:Species: Bacillus thuringiensis subsp. thuringiensis
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Oct-2004
C:Accession: S00873
R:Brizzard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2723-2724, 1988
A:Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus
A:Reference number: S00873; PMID:86203216; PMID:3362680
A:Accession: S00873
A:Molecule type: DNA
A:Residues: 1-1228 <BRI>
A:Cross-references: UNIPROT:P05517; UNIPARC:UPI0000126BDC; EMBL:X06711; NID:940264; PIDN
C:Gene: cryA4
A:Start codon: TTG
C:Superfamily: Parasporal crystal protein
C:Keywords: delta-endotoxin

Alignment Scores:
Pred. No.: 4,876-32 Length: 1228
Score: 607.00 Matches: 209
Percent Similarity: 40.32% Conservative: 114
Best Local Similarity: 26.09% Mismatches: 294
Query Match: 15.41% Indels: 184
DB: 2 Gaps: 35

US-10-782-570-1 (1-2235) x S00873 (1-1228)
Qy      1 GTGAATCAAAATTAATAATGAATATGATGATTCGATTATCGATTCAAGAAATTTATCTATCCT 60
      |||||
Db      1 MetThrSerAsnArgLysAsnGluAsnGluIleIleAsnAla-----Val 15
      |||||
Qy      61 TCTAAACAGAAATATTGATCATTTCTAGATACCCCTTACACAAATAATCCAAATCAACCAATTA 120
      |||||
Db      16 SerAsnHisSerAlaGlnMetAspLeuLeuPro----- 26
      |||||
Qy      121 CAAACACAAATTAACAAGAGGGCTCAATATGTGTCAAGGAATACACAAATATGATGAT 180
      |||||
Db      27 ---AspAlaArgIleGluAspSerLeuCysIleAlaGluGlyAsn----- 40
      |||||
Qy      181 AATTTTCGACATTTTGTAGTCTGATCAATTTGCTGAGTTAGTGCAGGTACTATTGTA 240
      |||||
Db      41 AsnIleAspProPheValSerAlaSerThr-----ValGlnThrGlyIleAsnIle 57
      |||||
Qy      241 TCCGGTACTCTGTAGCCGGTATAGTGGGCTCACTTCTATATCCGACCCGATAGGAATA 300
      |||||
Db      58 AlaGlyArgIleLeuGlyValLeuGly-----ValProPhe 69
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Qy      301 ATAGGTGCTATAATAATATCTTTTGGTACCCTAATCACTGCTCTTTTGGCCCGCGAGAA 360
      |||||
Db      70 AlaGlyGlnLeuAlaSerPheTyrSerPheLeuValGlyGluLeuTyrProArgGlyArg 89
      |||||
Qy      361 CAAGACAAAACAGATATGGACACAATTTATTAAATGGGAGAAATTTTGTGTATACACCG 420
      |||||
Db      90 AspGln-----TrpGluIlePheLeuGluHisValGluGlnLeuIleAsnGlnGln 106
      |||||
Qy      421 TTACACAGAAAGCATAAAACAGCTAAAGCTTAACTTACAAACTTTAGAGAGATTTAGACAAATATA 480
      |||||
Db      107 IleThrGluAsnAlaArgAsnThrAlaLeuAlaArgLeuGlnGlyLeuGlyAspSerPhe 126
      |||||
Qy      481 CAAAGCTTATTAATACAGCATTAGATGATTTGGAGAAAATTTAAAGACACTACAGCTCCTCGA 540
      |||||
Db      127 ArgAlaTyrGlnGlnSerLeuGluAspTrpLeuGlu-----AsnArgAspAsp 142
      |||||
Qy      541 TTACCACCATCATCAGCATTAACAACAGCTGCCTTGACTCTTAAAAATACGATTTTGAGAAT 600
      |||||
Db      143 AlaArgThrArgSerValLeuTyrThrGlnTyrIleAlaLeuGluLeu----- 158
      |||||
Qy      601 GTTCACAAATGATTTTATTCGAGAAATACCTGGTTCCAACTTGAACCTTATAAAACGCTA 660
      |||||
Db      159 -----AspPheLeuAsnAlaMetProLeuPheAlaIleArgAsnGlnGluValPro 175
      |||||
Qy      661 TTACTACTCTATTATGCGCAAGCTGCTAAATTTTTCATTTTAAATTTTATCAACAAGGTGCT 720
      |||||
Db      176 LeuLeuMetValTyrAlaGlnAlaAlaAsnLeuHisLeuLeuLeuLeuArgAspAlaSer 195
      |||||
Qy      721 GAATTTGGCTGATGAATGGAAATGCAGATATACATCTCTTCACAAAATTTGAACCTTAATGCTCGA 780
      |||||
Db      196 LeuPheGlySerGluPheGlyLeu----- 203
      |||||
Qy      781 ACATCAGATGAC-----TATTATAAACTTTTAAAGAAAATATACCTAATATATAGT 831
      |||||
Db      204 ThrSerGlnGluIleGlnArgTyrGluArgGlnValGluArgThrArgAspTyrSer 223
      |||||
Qy      832 AACTATTGTGCAAAATACCTATAGAGAGAGACTTAAATAAACTTCGAAACGAACCTAATATG 891
      |||||
Db      224 AspTyrCysValGluTyrTrpAsnThrGlyLeuAsnSerLeuArgGlyThrAsnAlaAla 243
      |||||
Qy      892 AGATGGAGATATATTAAATGATTATCGAAGATATATGACTATTACTGTATTAGATATATC 951
      |||||
Db      244 SerTrpValArgTyrAsnGlnPheArgArgAspLeuThrLeuGlyValLeuAspLeuVal 263
      |||||
Qy      952 GCTCAATTTCTTTTATGATATAAAGAGATACAAAGATTCATCAATGAGNAGATAGGTGCG 1011
      |||||
Db      264 AlaLeuPheProSerTyrAspThrArgThrTyrProIleAsn----- 277
      |||||
Qy      1012 ATTAATAACTGAACCTTACAGAGAAATTTATACA-----ACTGAATAAAT 1056
      |||||
Db      278 ThrSerAlaGlnLeuThrArgGluValTyrThrAspAlaIleGlyAlaThrGlyValAsn 297
      |||||
Qy      1057 TTTGACCGCTCTTACT---TACCTTTGAAATTCACCCCAATCTCGCTATATATGGAATATAT 1113
      |||||
Db      298 MetAlaSerMetAsnTrpTyrAsnAsnAsnAlaProSerPheSerAlaIleGluAlaAla 317
      |||||
Qy      1114 TTACACGCTTCAGGGCTTAGATATTTTTCATTTTTCATTTAGATGAACCTT---ATATTT 1164
      |||||
Db      318 AlaIleArgSerPro---HisLeuLeuAspPheLeuGluGlnLeuThrIlePheSerAla 336
      |||||
Qy      1165 -----TATACAAAATAATGAACCTTACGGGAAT 1191
      |||||
Db      337 SerSerArgTrpSerAsnThrArgHisMetThrTyrTrpArgGlyHisThrIleGlnSer 356
      |||||
Qy      1192 CGTTTAGTGTGATTTGCGAATCGTAATAGATCTACTTATGTCTACGACAGCAAGCTGAAAT 1251
      |||||
Db      357 ArgProIleGly---GlyGlyLeuAsnThrSerThrHisGlyAlaThrAsnThrSerIle 375
      |||||
Qy      1252 ATATATGAGAAAGAACACAGGTCCACCCACA-----ACAAAACCTTTAATACCA 1299
      |||||
Db      376 -----AsnProValThrLeuArgPheAlaSerArgAspValTyrArg 389
      |||||
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QY 1300 TTTGAATCTATAAGTTTCAATTGTAAGTATGATAGACAAGTAACCTCTACTTCCCTTTT 1359
Db 390 ThrGluSerTyrAlaGlyValLeuLeuTrpGlyIleTyrLeuGluProIleHieGlyVal 409
QY 1360 CCTACATACATCTATTACAAATTAATCAAATTTGAACCTTTATTTAAATAATACCTACCTAGTAAT 1419
Db 410 ProThrValArgPheAsnPhe-----ThrAsnProGlnAsn 421
QY 1420 AAATTAACATATTACGCTGGGGGAATTTATCTAATGATAAATAACCACTGATTTTCAA 1479
Db 422 -----IleSerAspArgGlyThrAlaAsnTyrSer 431
QY 1480 TTTCTGTGTAATA-----AAGACTGTAAACCAATTTAATCCCAAT 1521
Db 432 GlnProTyrGluSerProGlyLeuGlnLeuIleAspSerGluThrGluLeuProProGlu 451
QY 1522 TGTTTA-----CCAAGCTATAATATGATGATATTTATCCACAGTTCTTCTTTATTT 1575
Db 452 ThrThrGluArgProAsnTyrGluSerTyrSerHisArgLeuSerHisIleGlyIle 471
QY 1576 AATTAATCTATAAAATTTGGATTAGCGCTAAATATA-----TTATATACAGGTGCATTAGGA 1632
Db 472 LeuGlnSer-----ArgValAsnValProValTyrSer----- 482
QY 1633 TGGACACACAGTAGTTTAATAGAAATAATGCAATATCAGATATAAATAATTAATGATGTC 1692
Db 483 TrpThrHisArgSerAlaAspArgThrAsnThrIleGlyProAsnArgIleThrGlnIle 502
QY 1693 CCAGCAATCAAAGGTAAACAGTCTTGATACAAACTCTAAGGTAAATGGAAGGACCTGGTCAT 1752
Db 503 PrometValIleAlaSerGluLeuProGlnGlyThrThrValValArgGlyProGlyPhe 522
QY 1753 ACAGAGAGAACTTGGTTTATTCAAAAGTCAA-----GGCGCTTTAGAGATTACA 1803
Db 523 ThrGlyIleAspIleLeuArgArgThrAsnThrGlyIleGlyPheGlyProIleArgValThr 542
QY 1804 TGTGAACCTCTTAATCTTACCAATCTTATTACATTTAGACTTCGATACGCTACA----- 1857
Db 543 ValAsnGlyPro---LeuThrGlnArgTyrArgIleGlyPheArgTyrAlaSerThrVal 561
QY 1858 -----AATGGTCTCGAATACTCTTCTCAATATATATCTCTTACATA 1899
Db 562 AspPheAspPhePheValSerArgGlyGlyThrThrValAsnAsnPheArgPhe----- 579
QY 1900 CCAGAGTAATAGGAATACCACCTCAACGACTCAACAAACACTTTTCTGGTACAAATTAAT 1959
Db 580 -----LeuArgThrMetAsnSerGly----- 586
QY 1960 AATAATTTACATACGAGATTTTGGGTATTTCCAAATTTCCAACTACAGTACAGTAACATTACT 2019
Db 587 AspGluLeuIleTyrGlyAsnPheValArgAlaPheThrThr----- 601
QY 2020 TTAATCGAATAACATACCTATTTATATTTTAAATCGT---GCAGATGTA----- 2061
Db 602 -----ProPheThrPheThrGlnIleGlnAspIleIleArgThrSerIle 616
QY 2062 -----TCAATTTCAATTTAATCATTTGATAAATAATGATTTATACCAATTAAT 2109
Db 617 GlnGlyLeuSerGlyAsnGlyValTyrIleAspIleIleGlyIleIleProValThr 636
QY 2110 TCCTCTGTACGCCAAATAGAGAAAACAAAATTTAGAAACTATCTCCAAACAAAATAAAT 2169
Db 637 AlaThrPheGluAlaGluTyrAsp-----LeuGluArgAlaGlnGluAlaValAsn 653
QY 2170 ACATTTTTCACAAATCATACAAAAAATACTTTAATATAGAGCCACCAAACTATGATATT 2229
Db 654 AlaLeuPheThrAsnThrAsnProArgLeuLeuThrAspValThrAspTyrHisIle 673
QY 2230 GAT 2232
Db 674 Asp 674
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RESULT 12

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I39815
insecticidal protein cryV - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 05-Oct-2004
C:Accession: I39815
R:Gleave, A.P.; Williams, R.; Hedges, R.J.
Appl. Environ. Microbiol. 59, 1683-1687, 1993
A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for
Iensis subsp. kurstaki.
A:Reference number: I39815; MUID:93298009; PMID:8517758
A:Accession: I39815
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Releues: 1-719 <RES>
A:Cross-references: UNIPROT:Q45752; UNIPARC:UPI0000036008; GB:M98544; NID:G142767; PIDN:
C:Genetics:
C:Gene: cryV
C:Superfamily: Parasporal crystal protein

Alignment Scores:
Pred. NO.: 7.75e-31 Length: 719
Score: 588.50 Matches: 207
Percent Similarity: 40.23% Conservative: 112
Best Local Similarity: 26.10% Mismatches: 293
Query Match: 14.94% Indels: 181
DB: 2 Gaps: 34

US-10-782-570-1 (1-2235) x I39815 (1-719)
QY 43 AAGAAATTTATCTTATCTCTTAACAGAAATATTGATCAT---TCTAGATACCCCTTACACA 99
Db 8 LysHisGlnSerPheSerSerAsnAlaValAspLysIleSerThrAspSerLeuLys 27
QY 100 AATAATCCAATCAACATTACAAACACAAATTTACAAAGAGTGGCTCAATATGTGCAA 159
Db 28 AsnGluThrAspIleGluLeuGlnAsnIleAsnHisGluAspCysLeuLysMet----- 45
QY 160 GGGNATACAAATATGATGATTAATTCGACACATTTCTAGTGTGATACAAATTTGCTGCA 219
Db 46 -----SerGluTyr---GluAsnValGluProPheValSerAlaSerThrIleGln--- 61
QY 220 GTTAGTCAGGTACTATTGTATCGGTACTCTGTGTCGGTATAGTGGCTCACTTCT 279
Db 62 -----ThrGlyIleGlyIleAlaGlyLys 69
QY 280 ATATCCGACCGATAGGAATA-----ATAGGTGCTATAATAATATCTTTTGGTACCCTA 333
Db 70 IleLeuGlyThrLeuGlyValProPheAlaGlyGlnValAlaSerLeuTyrSerPheIle 89
QY 334 ATCACTCTCTTTGGCCCGGGGAGAACAGACAAACAGTATGACACAAATTTATATAA 393
Db 90 LeuGlyLeuLeuTrpProLysGly-----LysAsnGlnTrpGluIlePheMetGlu 106
QY 394 ATGGGAGAAATTTTGTGTATACACCCGTTAAACAGAAAGCATAAACAGCTAAAGTTACAA 453
Db 107 HisValGluGluIleIleAsnGlnLysIleSerThrTyrAlaArgAsnLysAlaLeuThr 126
QY 454 ACTTTAGAGGATTTAGACAAATATTACAAAGCTATTAATACAGCATTTAGATGATGG--- 510
Db 127 AspLeuLysGlyLeuGlyAspAlaLeuAlaValTyrHisAspSerLeuGluSerTrpVal 146
QY 511 -----NGAAATTTAAAGACTACAGCTCCCTGGATTACCACCATCATCAGCATTAACA 564
Db 147 GlyAsnArgAsnThrArgAlaArg-----SerValValLys 159
QY 565 CAAGCTCCCTTGACTCTTAAATACGATTTGAGAAATGTTTCAATGATTTTATTCGAGAA 624
Db 160 SerGlnTyrIleAlaLeuGluLeuMet-----PheValGlnLys 172
QY 625 ATACCTGTTTCCAACTTGAAACTTATPAAACGCTATTACTACTATTATTATTCGCAAGCT 684
Db 173 LeuProSerPheAlaValSerGlyGluGluValProLeuLeuProIleTyrAlaGlnAla 192
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Db 441 GlyTyrAlaGlyIleGlyThrGlnLeuGlnAspSerGluAsnGluLeuProGluAla 460
 Qy 1495 GACTGTAACCAATTAATTAATCAAAATGTTTACCAAGCTATAATAGTATAGTCAATAT 1554
 Db 461 ThrGlyGln-----ProAsnTyrGluSerTyrSerHisArg 472
 Qy 1555 TTATCCCAAGTTTCTTTATTAATTAATTCCTATAAATTTGGATTAGCCCTAAATATATTA 1614
 Db 473 LeuSerHisIleGlyLeuIleSerAlaSerHisValIysAlaLeuValTyrSer----- 490
 Qy 1615 TATACAGGTGCATTAGGATGACACACAGTGTGTTAATAGATAAATAAGCAATATCAGAT 1674
 Db 491 -----TyrThrHisArgSerAlaAspArgThrAsnThrIleGluPro 504
 Qy 1675 AAAATAATTACATGATCCCAAGCAATCAAGGTAAACAGCTTTGTGATGATAAACTTAAGGTA 1734
 Db 505 AsnSerIleThrGlnIleProLeuValIysAlaPheAsnLeuSerSerGlyAlaAlaVal 524
 Qy 1735 ATTGAAGACCTGGTCATACAGGAGAACTTGGTTTATTTTACAAAGTCAAGGG----- 1788
 Db 525 ValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrAsnThrGlyThrPhe 544
 Qy 1789 -----CGTTTAGAGATTACATGTAGAACTCTTAATTTCTACACAACTTTATTAACATT 1839
 Db 545 GlyAspIleArgValAsnIle-----AsnProProPheAlaGlnArgTyrArgVal 561
 Qy 1840 AGACTTCGATACGCTTACA-----AATGGTGTGGA 1869
 Db 562 ArgIleArgTyrAlaSerThrThrAspLeuGlnPheHisThrSerIleAsnGlyIysAla 581
 Qy 1870 AATACTCTTCCTATATATCTTACATATACCGAGGTAAAGGATACACCTCAACGA 1929
 Db 582 IleAsnGlnGlyAsnPheSerAlaThrMet----- 591
 Qy 1930 CTCACAACTTTTCTGGTACAAATTAATAATTTACATACCGAGATTTGGGTAT 1989
 Db 592 -----AsnArgGlyGluAspLeuAspTyrLysThrPheArgThr 604
 Qy 1980 TTCCAATTTCCAAGTACAGTAACTTACCTTTAAATCGAAACATACCACTTATTAAT 2049
 Db 605 ValGlyPheThr-----ProPheSerPhe--- 613
 Qy 2050 CGTCAGATGTATCAAAATCAATTTTATC----- 2079
 Db 614 ---LeuAspValGlnSerThrPheThrIleGlyAlaTrpAsnPheSerSerGlyAsnGlu 632
 Qy 2080 -----ATTGATAAAATTTGAATTTATACCAATTTACTCTCTGTACGCCAAATAGAGAA 2133
 Db 633 ValTyrIleAspArgIleGluPheValProValGluValThrTyrGluAlaGluTyrAsp 652
 Qy 2134 AAACAAAATTTAGAACTATCCAAACAAAATAATACATTTTTCACAAATCATACAAA 2193
 Db 653 -----PheGluIysAlaGlnGluIysValThrAlaLeuPheThrSerThrAsnPro 669
 Qy 2194 AATACCTTTAAATATAGACCCACAACTATGATTTGAT 2232
 Db 670 ArgGlyLeuLysThrAspValIysAspTyrHisIleAsp 682

RESULT 15
 S11446
 parasporal crystal protein cryIba1 - Bacillus thuringiensis
 A:Alternate names: parasporal crystal protein cryID
 C:Species: Bacillus thuringiensis
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Oct-2004
 C:Accession: S11446
 R:Hoefte, H.; Soetaert, P.; Janssens, S.; Referoen, M.
 Nucleic Acids Res. 18, 5545, 1990
 A:Title: Nucleotide sequence and deduced amino acid sequence of a new Lepidoptera-specific
 A:Reference number: S11446; MUID:91016042; PMID:2216728
 A:Accession: S11446
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1165 <HOB>

A:Cross-references: UNIPROT:P19415; UNIPARC:UPI000002COA3; EMBL:X54160; NID:940279; PIDN
 C:Superfamily: Parasporal crystal protein
 C:Keywords: Delta-endotoxin

Alignment Scores:
 Pred. No.: 5,08e-30 Length: 1165
 Score: 576.00 Matches: 198
 Percent Similarity: 42.49% Conservative: 119
 Best Local Similarity: 26.54% Mismatches: 275
 Query Match: 14.62% Indels: 154
 DB: 2 Gaps: 29

US-10-782-570-1 (1-2235) x S11446 (1-1165)

Qy 100 AATAATCAATCAACATTTACAAAACACAAATTTACAAAGAGTGGCTCAATATATGTGCAA 159
 Db 4 AsnAsnGlnAsnGlnCysValProTyrAsn-----CysLeu 15
 Qy 160 GGGNATACAAA-----TATGGTGATAAATTTCCGAGACATTTGCTAGTGTGATGATA 210
 Db 16 SerAsnProIysGluIleLeuLeuGlyGlu-----GluArgLeuGluThrGlyAsnThr 33
 Qy 211 ATTGCTCAGTTAGTCAGGTACTATT-----GTATCCGTACTCTGTAGCCGGTATA 264
 Db 34 ValAlaAspIleSerLeuGlyLeuIleAsnPheLeuTyrSerAsnPheValProGly--- 52
 Qy 265 GTGGGGTCACTTCTATATATCCGACCGATAGGAATAATAGTGTCTATAATAATATCTTTT 324
 Db 53 GlyGlyPhe-----IleValGly----- 58
 Qy 325 GTATCCCTTAATCACTGCTTTTGGCCCGCGGAGAACACAGCAAAACAGTATGACACAA 384
 Db 59 -----LeuLeuGluLeuIleTrp-----GlyPheIleGlyProSerGlnTrpAspIle 74
 Qy 385 TTTATTAATAATGGAGAGAAATTTTGTGTATACACCGTTAAACAGAGACATAAAACAGCTA 444
 Db 75 PheLeuAlaGlnIleGluGlnLeuIleSerGlnArgIleGluGluPheAlaAsnGln 94
 Qy 445 AAGTTACAACTTTAGAGGATTTAGACAAATATTACAAAGCTATATATACAGCATTAGAT 504
 Db 95 AlaIleSerArgLeuGluGlyLeuSerAsnLeuTyrLysValTyrValArgAlaPheSer 114
 Qy 505 GATTGGAGAAATTAATAAGACATACAGCTCTGGATTACCACCATCATCAGCATCAAA 564
 Db 115 AspTrpGluLys-----AspProThrAsnProAlaLeuArg 126
 Qy 565 CAAGCTCGCTTGACTCTTAATAATACGATTTGAGAATGTTCCACATGATTTTATTCGAGAA 624
 Db 127 Glu-----GluMetArgIleGlnPheAsnAspMetAsnSerAlaLeuIleThrAla 143
 Qy 625 ATACCTGGTTTCCAACTTGAACCTTATAAAACGCTATTACTACCTATTATTCGCAAGCT 684
 Db 144 IleProLeuPheArgValGlnAsnTyrGluValAlaLeuLeuSerValTyrValGlnAla 163
 Qy 685 GCTAATTTTCAATTAATTTATTAACAAGGTGCTCAATTTGGCTGATGAATGAATGCA 744
 Db 164 AlaAsnLeuHisLeuSerIleLeuArgAspValSerValPheGlyGluArgTrpGlyTyr 183
 Qy 745 GATATACATCTCTTACAAATTTGAACCTTAATGCTGGAAACATCAGATGACTATTATAAATT 804
 Db 184 Asp-----ThrAlaThrIleAsnAsnArgTyrSerAsp 194
 Qy 805 TTTAAAGAAATATATACCTAATATATAGTAATTTGTGCAATATACCTATAGAGAGGACTA 864
 Db 195 LeuThrSerLeuIleHisValTyrThrAsnHisCysValAspThrTyrAsnGlnGlyLeu 214
 Qy 865 AATAAATCTCGAAACGACCTAATATGAGATGGAGTATATTATGATTTATCGAAGATAT 924
 Db 215 ArgGluLeuGluGlyArgPheLeuSerAspTrpIleValTyrAsnArgPheArgArgGln 234
 Qy 925 ATGACTATTACTGTATTAGATATCTATCGCTCAATTTTCTTTTATGATATAAGAGATAC 984
 Db 235 LeuThrIleSerValLeuAspIleValAlaPhePheProAsnTyrAspIleArgThrTyr 254

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QY 985 AAAGATTCAATAGGAAGTAAGTGGCATTAATAAAGTGAACCTTACAGAGAAATTTATACA 1044
Db 255 ProIleGlnThrAla-----ThrGlnLeuThrArgGluValTyr--- 267
QY 1045 ACTGAATAAATATTTT-----GACCGTCTTACTTACTTGAATAATCAACCCAAATCCGCT 1098
Db 268 LeuAspLeuProPheIleAsnGluAsnLeuSerProAlaAlaSerTyrProThrPheSer 287
QY 1099 ATAATGGGAATATAATTAACAGCTTCAGGGCTTAGAATTAATTTTCATTTTGTAGTAACACTT 1158
Db 288 AlaAlaGluSerAlaIleIleArgSerPro---HisLeuValAspPheLeuAsnSerPhe 306
QY 1159 ATATTTTATACAAAAAATGAAACGTAGCGGAATCGTTTGGTATTGCGGAATCGTAAT 1218
Db 307 ThrIleTyrThrAsp-----Ser 312
QY 1219 AGATCTACTTATGCTACGACGAGAACTGAAATTAATATATATATGAGAAAGAACAGGTCCACCC 1278
Db 313 LeuAlaArgTyrAlaTyrTrpGlyGlyHisLeuValAsnSerPheArgThrGly----- 330
QY 1279 ACAACAAAACTTTAATACCATTTGAACTTAAAGTTTCAATTTGTAACTGATAGACAA 1338
Db 331 ThrThrThrAsnLeuIleArgSerProLeuTyrGlyArgGluGlyAsnThrGluArgPro 350
QY 1339 GTAACTCTCTACT---TCCCTTTTCTTAACATATACTTTTACAAATTAATCAAAATTCGAAT 1395
Db 351 ValThrIleThrAlaSerProSerValProIlePheArgThrLeuSerTyrIleThrGly 370
QY 1396 TATTTAAATTAATTCACCTAGTAATAAATTAACATATTCAGCTGGGGGGAATTTATCTAAT 1455
Db 371 LeuAspAsnSerAsnProValAlaGlyIle----- 380
QY 1456 GATAAAAAAACAACTGATTTTCAATTTCTGTAAAAAAGAC-----TGTAAA 1503
Db 381 -----GluGlyValGluPheGlnAsnThrIleSerArgSerIleTyrArgLysSerGly 398
QY 1504 CCAATTTATTAATCCAAATTTGTTTACCAGCTATATAGT----- 1542
Db 399 ProIleAspSerPheSerGluLeuProProGlnAspAlaSerValSerProAlaIleGly 418
QY 1543 TATAGTCATATTTATCCAGTTTCTTTTATTTAATTTCTTATAAATAATGGATTAGCG 1602
Db 419 TyrSerHisArgLeuCyHisAlaThrPheLeuGluArgIleSerGlyProArgIleAla 438
QY 1603 CTAATATATTTATATACAGGTGCATTAGGATGGACACACAGTAGTGTATTAAGAAATAT 1662
Db 439 GlyThrVal-----PheSerTrpThrHisArgSerAlaSerProThrAsn 453
QY 1663 GCAATATCAGATAAATAATTAATTAATCAATCCAGCAATCAAAAGGTAACAGTCTTGATACA 1722
Db 454 GluValSerProSerArgIleThrGlnIleProTrpValLysAlaHisThrLeuAlaSer 473
QY 1723 AACTCTAAGGTAATGAAGGACTGGTCAATACAGGAGAACTTGGTTTATTTTACAAAGT 1782
Db 474 GlyAlaSerValIleLysGlyProGlyPheThrGlyGlyAspIleLeuThrArgAsnSer 493
QY 1783 CAAGGG-----CGTTTAGAGATTACATGTAGAACTCTTAATTTCTACACAA 1827
Db 494 MetGlyGluLeuGlyThrLeuArgValThrPheThrGlyArgLeuPro-----Gln 510
QY 1828 TCCTATTACATTAAGACTTCGATACGCTACA-----AATGGTGTGGA----- 1869
Db 511 SerTyrTyrIleArgPheArgTyrAlaSerValAlaAsnArgSerGlyThrPheArgTyr 530
QY 1870 AATFACTCTTCTAATATATCTCTTACATACAGGAGTAATAGGAATACCACCTCAACGA 1929
Db 531 SerGlnProProSerTyrGlyIleSerPheProLysThrMetAspAlaGlyGluProLeu 550
QY 1930 CTCACAAACACTTTTCTGGTACAAATTAATAATTTACAATACGAGATTTTGGGTAT 1989
Db 551 ThrSerArgSerPheAlaHisThrThrLeuPheThr----- 562
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QY 1990 TTCCAATTTCCAAGTACAGTAACATTACCTTTAAATCGAAACATACCACTTTATATTTAAT 2049
Db 563 -----ProIleThrPheSer 567
QY 2050 CGTCAGATGTATCAAAATTCAAATTTTAATC-----ATTGATAAAATTGAA 2094
Db 568 ArgAlaGlnGluGluPheAspLeuTyrIleGlnSerGlyValTyrIleAspArgIleGlu 587
QY 2095 TTTATACCAATTTACTTCTCTGTAGCGCAAAATAGAGAAAAACAAAAATTAGAAAATATC 2154
Db 588 PheIleProValThrAlaThrPheGluAlaGluTyrAsp-----LeuGluArgAla 604
QY 2155 CAAACAAAAATAAATACATATTTTTCACAAATCATACAAAAAATACCTTTAAATATAGAAAGCC 2214
Db 605 GlnLysValValAsnAlaLeuPheThrSerThrAsnGlnLeuGlyLeuLysThrAspVal 624
QY 2215 ACAAACTATGATTTGAT 2232
Db 625 ThrAspTyrHisIleAsp 630
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Search completed: January 12, 2006, 06:42:48
Job time : 86.5 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 12, 2006, 06:15:49 ; Search time 241.5 Seconds
(without alignments)
13058.847 Million cell updates/sec

Title: US-10-782-570-1
Perfect score: 3939
Sequence: 1 gtgaatcaaaataataa.....caaatgatattgattataa 2235

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ncp.model p/US10782570/runat_12012006_060221_7515/app.query.fasta_1.2375
-Q=/cgm2_1/USPTO_epool_p/US10782570/runat_12012006_060221_7515/app.query.fasta_1.2375
-DB=Uniprot -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=500 -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10782570@cgm_1_1_418 @runat_12012006_060221_7515 -NCFU=6 -ICFU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRAD=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOF=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot_05.80.*

1: uniprot_eprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1158	29.4	1180	1 CR4AA_BACTI	P16480 bacillus th
2	1158	29.4	1180	2 Q7AL67_BACTI	Q7AL67 bacillus th
3	906.5	23.0	1128	2 Q9FDC0_BACTF	Q9FDC0 bacillus th
4	901	22.9	1109	1 C28AA_BACTF	Q9x682 bacillus th
5	897	22.8	675	1 C10AA_BACTI	P09662 bacillus th
6	897	22.8	675	2 Q8KNV2_BACTI	Q8KNV2 bacillus th
7	842.5	21.4	650	2 Q8VNX2_BACTV	Q8VNX2 bacillus th
8	819	20.8	1136	1 CR4BA_BACTI	P05519 bacillus th
9	819	20.8	1136	2 Q7AL72_BACTI	Q7AL72 bacillus th
10	801.5	20.3	688	2 Q8VNX1_BACTV	Q8VNX1 bacillus th
11	796	20.2	683	2 Q75VA2_BACTE	Q75VA2 bacillus th
12	787.5	20.0	1169	1 CR8BA_BACTE	Q45705 bacillus th
13	755.5	19.2	688	2 Q5W7N9_BACTU	Q5W7N9 bacillus th
14	709	18.0	682	1 C19BA_BACTH	Q86170 bacillus th
15	708.5	18.0	1169	2 Q56B08_BACTU	Q56B08 bacillus th
16	706	17.9	659	1 CR3BA_BACTO	P17969 bacillus th

17	699	17.7	829	2	Q6BE06_BACTU	Q6BE06 bacillus th
18	691	17.5	652	1	CR3BB_BACTU	Q06117 bacillus th
19	689	17.5	648	1	C19AA_BACTU	Q32307 bacillus th
20	689	17.5	1138	1	CR7AB_BACTU	Q45708 bacillus th
21	688	17.5	1138	1	CR7AA_BACTU	Q3749 bacillus th
22	686.5	17.4	660	2	Q8RQU6_BACTA	Q8RQU6 bacillus th
23	686	17.4	825	2	Q6BE09_BACTU	Q6BE09 bacillus th
24	682.5	17.3	1236	2	Q939T3_BACTU	Q939T3 bacillus th
25	680	17.3	1280	2	Q8VUK9_BACTU	Q8VUK9 bacillus th
26	677.5	17.2	1157	1	CR8AA_BACTU	Q45704 bacillus th
27	672	17.1	1160	1	CR8CA_BACTP	Q45706 bacillus th
28	672	17.1	1160	2	Q6RZK6_BACTU	Q6RZK6 bacillus th
29	661	16.8	1138	1	CR7AB_BACTU	Q45707 bacillus th
30	659.5	16.7	686	2	Q75Q05_BACTE	Q75Q05 bacillus th
31	655.5	16.6	1157	1	CR9CA_BACTO	Q759G5 bacillus th
32	654.5	16.6	1163	2	Q5XLA8_BACTP	Q5XLA8 bacillus th
33	652	16.6	1169	1	CR9DA_BACTP	Q06014 bacillus th
34	636.5	16.2	1144	2	Q8KZL7_BACTG	Q8KZL7 bacillus th
35	635	16.1	1154	2	Q6QAN9_BACTG	Q6QAN9 bacillus th
36	631	16.0	1254	2	Q8VUL0_BACTU	Q8VUL0 bacillus th
37	630	16.0	826	1	C27AA_BACTH	Q8A597 bacillus th
38	625	15.9	1150	1	CR9EA_BACTA	Q8ZNL9 bacillus th
39	625	15.9	1150	2	Q71RF4_BACTU	Q71RF4 bacillus th
40	623.5	15.8	1231	2	Q8KNY2_BACTU	Q8KNY2 bacillus th
41	620	15.7	1340	2	Q589X2_PAEPP	Q589X2 paenibacill
42	620	15.7	1344	2	Q765X7_9BACL	Q765X7 paenibacill
43	616.5	15.7	644	1	CR3AA_BACTD	P0A381 bacillus th
44	616.5	15.7	644	1	CR3AA_BACTM	P0A380 bacillus th
45	616.5	15.7	644	1	CR3AA_BACTT	P0A379 bacillus th

ALIGNMENTS

RESULT 1	CR4AA_BACTI	STANDARD;	PRT;	1180 AA.
ID	CR4AA_BACTI			
AC	P16480;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Pesticidal crystal protein cry4Aa (insecticidal delta-endotoxin			
DE	CryIVA(a)) (crystalline entomocidal protoxin) (135 kDa crystal			
DE	protein).			
GN	Name=cry4Aa; Synonyms=cryIVA(a), isxH4;			
OS	Bacillus thuringiensis subsp. israelensis.			
OG	Plasmid 72 Kb.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;			
OX	Bacillus cereus group.			
OX	NCBI_TaxID=1430;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Sen K., Honda G., Koyama N., Nishida M., Neki A., Sakai H., Himeno M.,			
RA	Komano T.;			
RT	"Cloning and nucleotide sequences of the two 130 kDa insecticidal			
RT	protein genes of Bacillus thuringiensis var. israelensis.";			
RL	Agric. Biol. Chem. 52:873-878(1988).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=88015571; PubMed=2821500;			
RA	Ward E.S., Ellar D.J.;			
RT	"Nucleotide sequence of a Bacillus thuringiensis var. israelensis gene			
RT	encoding a 130 kDa delta-endotoxin.";			
RL	Nucleic Acids Res. 15:7195-7195(1987).			
RN	[3]			
RP	MUTAGENESIS STUDIES.			
RX	MEDLINE=94307434; PubMed=7913448; DOI=10.1016/0014-5793(94)00604-0;			
RA	Nishimoto T., Yoshigae H., Ihara K., Sakai H., Komano T.;			
RT	"Functional analysis of block 5, one of the highly conserved amino			
RT	acid sequences in the 130-kDa CryIVA protein produced by Bacillus			
RT	thuringiensis subsp. israelensis.";			
RL	FEBS Lett. 348:249-254(1994).			
CC	-!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut			
CC	epithelial cells of insects.			


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QY 1525 TTACCAAGCTAATAGTTAGTGCATATTTATCCAGTTTCTTTTATTAATTAT--- 1581
Db 491 PheProThrTyraAsnSerHisLeuSerPheLeuSerLeuSerLeuPro 510
QY 1582 ---TCTATAAAATGGATTAGCGCTAAATATATATATATATACAGGTGCATTAGGATGGACA 1638
Db 511 AlaThrTyraLys-----ThrGlnValTyraPheAla-----TrpThr 523
QY 1639 CACAGTAGTTTATAGAAATAATGCAATATCAGATAAAATAATATACATGATCCAGCA 1698
Db 524 HisSerSerValAspProLysAsnThrIleTyraHisLeuThrGlnIleProAla 543
QY 1699 ATCAAAGGTAAACAGCTTGATACAACTCTAAGGTAATTTGAAGGACCTGGTCATACAGCA 1758
Db 544 ValIleAlaAsnSerLeuGlyThrAlaSerIleValGlnGlyProGlyHisThrGly 563
QY 1759 GGAACCTGGTTTATTTACAAAGTCNAGGGCGTTTATAGAGATTACATGATAGAACTCCTAAT 1818
Db 564 GlyAspLeuLeu-----AspPheLysAspHisPheLysIleThrCysGlnHisSerAsn 581
QY 1819 TCTACAACTTATATACATTAGACTTCGATACCGCTACAAATAGTGCTGGAAATACCTCTT 1878
Db 582 PheGlnGlnSerTyraPheIleArgIleArgTyraLysAsnGlySerAlaAsnThrArg 601
QY 1879 CCTAATATATCTTACAACTACAGGAGTAATAGGAATACCACTCAACGACTCAACAAC 1938
Db 602 AlaValIleAsnLeuSerIleProGlyValAlaGluLeu---GlyMetAlaLeuAsnPro 620
QY 1939 ACTTTTCTGGTCAAAATTAATTAATTTACAATACGGAGATTTTGGGTATTTCCAATTT 1998
Db 621 ThrPheSerGlyThrAspTyraHisLeuLysTyraLysAspPheGlnTyraLeuGluPhe 640
QY 1999 CCAAGTACAGTAACATTAATCTTTAATCGAAACATACCAATTAATTAATTAATTAATTAAT 2058
Db 641 SerAsnGluValLysPheAlaProAsnGlnAsnIleSerLeuValPheAsnArgSerAsp 660
QY 2059 GTA---TCAAAATCAATTTAATCATATGATAAAATTTGAATTTATACCAATTAATTAAT 2115
Db 661 ValTyraHisThrThrValLeuIleAspTyraLysGluPheLeuProIleThrArgSer 680
QY 2116 GTACGCCAAATAGAGAAACAAATAATAGAAATCTCCAAACAAATAATTAATTAATTAAT 2175
Db 681 IleArgGluAspArgGluLysGlnLysLeuGluThrValGlnGlnIleLeuAsnThrPhe 700
QY 2176 TTCACAAATCATACAAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2232
Db 701 TyraLysProIleLysAsnThrLeuGlnSerGluLeuThrAspTyraAspIleAsp 719

RESULT 2
Q7AL67_BACTI PRELIMINARY; PRT; 1180 AA.
AC Q7AL67;
DT 10-WAY-2005. (TrEMBLrel. 30, Created)
DT 10-WAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-WAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Pesticidal crystal protein cry4AA.
GN Name=cry4AA; Synonyms=cryIVA(A), isrH4, pBt110;
OS Bacillus thuringiensis (subsp. israelensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1430;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22235415; PubMed=12324359;
RX DOI=10.1128/AEM.68.10.5082-5095.2002;
RA Betty C., O'Neil S., Ben-Dov E., Jones A.P., Murphy L., Quail M.A.,
RA Harris D., Zaritsky A., Parkhill J.,
RT "Complete sequence and organisation of ptoxis, the toxin-coding
RT plasmid of Bacillus thuringiensis subsp. israelensis.";
RL Appl. Environ. Microbiol. 68:5082-5095(2002).
DR EMBL; AL731825; CAD30148.1; -; Genomic DNA.
SQ SEQUENCE 1180 AA; 134538 MW; 6FB5B56979DACAD3B CRC64;
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Alignment Scores:
Pred. No.: 5,16e-70 Length: 1180
Score: 1158.00 Matches: 283
Percent Similarity: 54.55% Conservative: 131
Best Local Similarity: 37.29% Mismatches: 281
Query Match: 29.40% Indels: 64
DB: 2 Gaps: 25

US-10-782-570-1 (1-2325) x Q7AL67_BACTI (1-1180)
QY 13 AATAATAATGAATATGAGATTATCGATTCA-----AGAATTTATCTTATCTCTTCTAAC 66
Db 6 AsnLysAsnGluTyraGluThrLeuAsnAlaSerGlnLysLysLeuAsnIleSerAsnAsn 25
QY 67 AGAAATATTGATCATCTTAGATACCTTACACAATATCCAAATCAACCATCAACAAAC 126
Db 26 -----TyrThrArgTyraProIleGluAsnSerProLysGlnLeuGlnSer 41
QY 127 ACAATTAACAAGAGTGGCTCAATATGTCTCAAGGAATACACAATATGATGATATTC 186
Db 42 ThrAsnTyraLysAspTrpLeuAsnMetCysGlnGlnAsnGlnGlnTyraGlyAspPhe 61
QY 187 GAGACATTTGCTAGTCTGATACAAATGCTGCTGAGTTAGTGCAGGTACTTATGTCGGT 246
Db 62 GluThrPheIleAspSer-----GlyGluLeuSerAlaTyraThrIleValValGly 78
QY 247 ACTCTGTTAGCCGCTATAGTGGGCTCACTTCTATATCCGACCGATAGGAATATAGT 306
Db 79 ThrValLeuThrGlyPheGlyPheThr-----ProLeuGlyLeu----- 92
QY 307 GCTATAATAATATCTTTTGGTACCTTAATCACTGCTCTTTGGCCCGCGGAGAACAGAC 366
Db 93 ---AlaLeuIleGlyPheGlyThrLeuIleProValLeuPheProAlaGlnAspGlnSer 111
QY 367 AAAACAGTATGGACACAATTTTATAAATGGGAGAAATTTTGTGTATACACCGTTAACA 426
Db 112 AsnThr---TrpSerAspPheIleThrGlnThrLysAsnIleIleLysLysGluIleAla 130
QY 427 GAAAGCATAAACAGCTAAAGTTACAACTTAGAGGATTTAGACAAATATTACAAAGC 486
Db 131 SerThrTyraIleSerAsnAlaAsnLysIleLeuAsnArgSerPheAsnValIleSerThr 150
QY 487 TATAATACAGCATATAGATGATTGGAGAAAATTTAAAGACTCAAGCTCTCGATTACCA 546
Db 151 TyrHisAsnHisLeuLysThrTrpGlu-----AsnAsnProAsnProGln 165
QY 547 CCATCATCAGCATTTACAAACAGCTGCTTGAATCTTAAATACGATTTGAGAAATGTTAC 606
Db 166 AsnThrGlnAspValArgThrGlnIleGlnLeuValHisTyraHisPheGlnAsnValIle 185
QY 607 AATGATTTTATTCGAGAAATACCT-----GGTTTCCAATTTGAACCTTATAAAGCTTA 660
Db 186 ProGluLeuValAsnSerCysProAsnProSerAspCysAspTyraThrAsnLeuLeu 205
QY 661 TTACTACCTATTATTCGCAAGCTGCTAATTTTCAATTTTAAATTTTATTAACAAGGTGCT 720
Db 206 ValLeuSerSerTyraGlnAlaAlaAsnLeuHisLeuThrValLeuAsnGlnAlaVal 225
QY 721 GAAATGGCTGATGAATGGAATGCAGATATACATCTTCAAAATTTGAACCTTAATGCTGA 780
Db 226 LysPheGluAlaTyraLysAsnAsnArgGlnPheAspTyraLeuGluPro---LeuPro 244
QY 781 ACATCAGATGATATTAATAACTTTTAAAGAAATATACCTTAATATAGTAACTATTGCT 840
Db 245 ThrAlaIleAspTyraTyraProValLeuThrLysAlaIleGluAspTyraThrAsnTyraCys 264
QY 841 GCABAATCTATAGAGAGGACTAAATAAACTTCGAAACGAACT----- 885
Db 265 ValThrThrTyraLysGlyLeuAsnLeuIleLysThrProAspSerAsnLeuAsp 284
QY 886 ---AATATGAGATGGAGTATATTTAATGATTATCGAAGATATATGATTAATGATTA 942
Db 886 ---AATATGAGATGGAGTATATTTAATGATTATCGAAGATATATGATTAATGATTA 942
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Db 285 GlyAsnIleAsnThrTyrAsnThrTyrArgThrLysMetThrAlaValLeu 304
QY 943 GATACATCGCTCAATTTCTTTTATGATATAGAGATACAAAGATTCAATAGGAAGA 1002
Db 305 AspLeuValAlaLeuPheProAsnTyrAspValGlyLysTyrProIle----- 320
QY 1003 ATAGGTGGCATTAAACAGTCACTACAGAGAAATTTATACAACTGAATAAATTTTCAC 1062
Db 321 -----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal---LeuAsnPheGlu 337
QY 1063 CGTCTTACTTACTTGAATCAACCCCAATCTCGCTAATAATGGAATATAATTAACAGT 1122
Db 338 GluSerProTyrLysTyrTyr-----AspPheGlnTyrGlnGluAspSerLeuThrArg 355
QY 1123 TCAGGGCTAGATTTTCTATTTTATAGTGAACCTTATATATTTTATACAAAATAAGAACG 1182
Db 356 ArgPro----HisLeuPheThrTrpLeuAspSerLeuAsnPheTyrGluLysAlaGlnThr 374
QY 1183 TACGGGAATCGTTAGTTGGTATTCGGAATCGTAAATAGATCTACTTATGCT----- 1233
Db 375 ThrProAsnAsnPhePhe----ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn 393
QY 1234 ACACAGCAAGTCAATATATATATGAGAGAAAGACAGGTCCACCCACAAACAAACTTTA 1293
Db 394 IleSerGlnLysSerSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu 413
QY 1294 ATACATTTGAATCTATTAAGTTTCAATTTGAATCTGATAGACAAAGTAACTCTACTTCC 1353
Db 414 -----GlyLeuAlaThrAsnIleTyrIlePheLeuLeuAsnValIleSerLeuAspAsn 431
QY 1354 CTTTTCCTAACATATCTTCAATTAATCAATTTGAATCTTATTAATAATTAATCACT 1413
Db 432 LysTyrLeuAsnAspTyrAsnAsnIleSerLysMetAspPhePheIleThrAsnGlyThr 451
QY 1414 -----AGTAATAAATTAACTATTTCACTGGGGGAATTTATCTAATGATAAATAA 1464
Db 452 ArgLeuLeuGluLysGluLeuThr---AlaGlySerGlyGlnIleTyrAspValAsn 470
QY 1465 ACACTGATTTCAATTTCTGTAAAGAAAGACTGTAACCAATTTAATCCAAATGT 1524
Db 471 LysAsnIlePheGlyLeuProIleLeuLysArgGluAsnGlnGlyAsnProThrLeu 490
QY 1525 TTACCAAGCTAATAAGTATAGTATATTTATCCAGTTTCTTTTATTTAATAT--- 1581
Db 491 PheProThrTyrAspAsnTyrSerHisIleLeuSerPheIleLysSerLeuSerIlePro 510
QY 1582 ---TCCTATAAATTTGGATTACGCTAATATATATATATATACAGGTGCATAGGACGA 1638
Db 511 AlaThrTyrLys-----ThrGlnValTyrThrPheAla-----TrpThr 523
QY 1639 CACAGTGTGTTAATAAGAAATATCAATATCAGATAAATAATTAATGATATCCAGCA 1698
Db 543 HisSerSerValAspProLysAsnThrIleTyrThrHisLeuThrThrGlnIleProAla 543
QY 1699 ATCAAAGTAAACAGCTTGTGATCAAACTCTAAGGTAATTAAGGACCTGGTGCATACAGGA 1758
Db 544 ValLysAlaAsnSerLeuGlyThrAlaSerLysValValGlnGlyProGlyHisThrGly 563
QY 1759 GGAACTTGGTTTATTTTCAAAAGTCAAGGGCGTTTGAAGATTACATGATAGAACCTCTAAT 1818
Db 564 GlyAspLeuIle-----AspPheLysAspHisPheLysIleThrCysGlnHisSerAsn 581
QY 1819 TCTACACATCTTATATACATTAGCTTCGATACGCTCAAAATGGTGTGCGAATACTCTT 1878
Db 582 PheGlnGlnSerTyrPheIleArgIleArgTyrAlaSerAsnGlySerAlaAsnThrArg 601
QY 1879 CCTAATATCTCTTACAAATCCAGAGTAATAGGAATACCACCTCAACGACTCAACAC 1938
Db 602 AlaValIleAsnLeuSerIleProGlyValAlaGluLeu----GlyMetAlaLeuAsnPro 620
QY 1939 ACTTTTCTGGTACAAATATATATTAATTAACAATCGGAGATTTTGGGTATTTCCAAATT 1998
Db 621 ThrPheSerGlyThrAspTyrThrAsnLeuLysTyrLysAspPheGlnTyrLeuGluPhe 640

QY 1999 CCAAGTACAGTAACTACCTTTAAATCGAAACATACCAATTTATATTAATCGTCAGAT 2058
Db 641 SerAsnGluValLysPheAlaProAsnGlnAsnIleSerLeuValPheAsnArgSerAsp 660
QY 2059 GTA---TCAAATCAATTTTAATCATTTGATAAAATTAATTAATTAATTAATTAATTAAT 2115
Db 661 ValTyrThrAsnThrValLeuIleAspLysIleGluPheLeuProIleThrArgSer 680
QY 2116 GTACGCCAAATAGAGAAAAACAAAAATAGAACTATAGAACCAACAAATAAATACATTT 2175
Db 681 IleArgIleAspArgGluLysGlnLysLeuGluThrValGlnGlnIleIleAsnThrPhe 700
QY 2176 TTCACAATCATACAAAAATACCTTTAAATATAGAACCAACCAATATGATATTTGAT 2232
Db 701 TyrAlaAsnProIleLysAsnThrLeuGlnSerGluLeuThrAspTyrAspIleAsp 719
RESULT 3
Q9FDC0_BACTP
ID Q9FDC0_BACTP PRELIMINARY; PRT; 1128 AA.
AC Q9FDC0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Paraaporal inclusion protein Cry.
GN Name=Cry;
OS Bacillus thuringiensis (subsp. finitimus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=29337;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Moore G.D., Debro J.H.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF285775; AAC00235.1; -, Genomic_DNA.
DR HSP; Q06117; IJ16.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR SEQUENCE 1128 AA; 127450 MW; 61B0DC9454BDF0E8 CRC64;
Alignment Scores:
Pred. No.: 5,79e-53 Length: 1128
Score: 906.50 Matches: 245
Percent Similarity: 49.44% Conservative: 108
Best Local Similarity: 34.31% Mismatches: 242
Query Match: 23.01% Indels: 119
DB: 2 Gaps: 28
US-10-782-570-1 (1-2235) x Q9FDC0_BACTP (1-1128)
QY 199 AGTGTGATCAATTTGTCGAGTTAGTCAGGTACTATTGTATCGGTACTCTGTAGCC 258
Db 28 SerSerAspThrValAlaValValSerAlaGlyIleValValValGlyThrIleLeuThr 47
QY 259 GGTATAGTGGGTCACTTCTATATCCGGACCGATAGGAATAATAGTGTCTATAATAATA 318
Db 48 -----AlaPheAlaSerPheValAsnPro-----GlyValValLeuIle 60
QY 319 TCTTTTGGTACCTTAATCACTGCTTTTGGCCCGGGAGAACAGAC---AAACAGTA 375
Db 61 SerPheGlyThrLeuAlaProValLeuTrpProAspProGluGluAspProLysLysIle 80
QY 376 TGGACACAAATTTAATAAATGGGAGAAATTTTGTGTGATACACCGTTTAACAGAAAGCAT 435

Db 81 TrpSerGlnPheMetLysHisGlyLeuAspLeuLeuAenGlnThrIleSerThrAlaVal 100
Qy 436 AAACAGCTAAAGTTACAACTTTAGACGATTTAGACAAATATATACAAAGCTATAATACA 495
Db 101 LysGluIleAlaLeuAlaHisLeuAenGlyPheLysAspValLeuThrTyrrGluArg 120
Qy 496 GCATTAGATGATTGGAGAAATTAATAAGACTACAAAGCTCCGGATTACCAACCATCATCA 555
Db 121 AlaPheAenAspTrpLysArg-----AsnProSerAla 131
Qy 556 GCATTACAAACAGCTGCCTGACTCTTAAATATACGATTTGAGAAATGTTCAACATGATTTT 615
Db 132 -----AsnThrAlaArgLeuValSerGlnArgPheGluAenAlaHisPheAenPhe 148
Qy 616 ATTCGAGAAATACCTGGTTTCCAACTTAAACCTTATAAACCGCTATTACTACTACTATTAT 675
Db 149 ValSerAenMetProGlnLeuLeuProThrTyrrAspThrLeuLeuLeuSerCysTyrr 168
Qy 676 GCGCAAGCTGCTAAATTTTCATTAAATTTATTAACAAGGTGCTGGAATTTGGCTGATGAA 735
Db 169 ThrGluAlaAlaAenLeuHisLeuAenLeuLeuHisGlnGlyValGlnPheAlaAspGln 188
Qy 736 TCGAATGAGATATACATCTCTTCAAAATTTGAACCTAATGCTGGAAATCAGATGACTAT 795
Db 189 TrpAenAlaAspGlnProHisSerProMetLeuLysSerSerGlyThr-----Tyr 205
Qy 796 TATAAATTTTAAAGAAATATACCTAAATATATAGTAACTATGTCGAAATACCTATAGA 855
Db 206 TyrAspGluLeuLeuValTyrrIleGluLysTyrrIleAenTyrrCysThrLysThrTyrrHis 225
Qy 856 GAAGACTAAATTAATTCGAAACCAAGCTAATATGAGATGAGTATATTAATGATTTAT 915
Db 226 LysGlyLeuAenHisLeuLysGluSerGluLysIleThrTrpAspAlaTyrrAsnThrTyrr 245
Qy 916 CGAAGATATAGACTATATCTGTATATAGTATCTATCGCTCAATTTCTTTTATGATATA 975
Db 246 ArgArgGluMetThrLeuIleValLeuAspLeuValAlaThrPheProPheTyrrAspIle 265
Qy 976 AAGAGATACAAGATTCAATAGGAATAGTGGCATTAAACCTGAACCTTACAGAGAA 1035
Db 266 ArgArgPhePro-----ArgGlyValGluLeuGluLeuThrArgGlu 279
Qy 1036 ATTTATACAACT-----GAAATAAATTTT 1059
Db 280 ValTyrrThrSerLeuAspProProGlyLeuAenAlaGlyProIleProGluIleAspPhe 299
Qy 1060 GACCGCTTACTTACTCTTGAATTCACCCCAATCTCGCTATATAGATGAATATAATTAACA 1119
Db 300 -----SerTyrrLeuGluAspHisLeuThr 307
Qy 1120 CGTTCAGGCTTAGATTTATTTTCATTTTGTAGATGAATTTATTTATATACAAATAATGAA 1179
Db 308 ArgProPro-----GlyLeuPheThrTrpLeuSerAspIleGluLeuTyrrThrGluSerVal 326
Qy 1180 ACGTACGGAAATCGTTTGTATGCGAATCGTAATAGATCTACTTACTTATGCTACGACA 1239
Db 327 AlaGluGlyAspTyrrLeuSerGlyIle-----ArgGluSerLysTyrrTyrrThr 342
Qy 1240 GGAACCTGAATTT-----ATATATGAGAAAGAACAGGTCCACCCCAACA 1284
Db 343 GlyAenGlnPhePheThrMetLysAenIleTyrrGlyAen-----ThrAen 357
Qy 1285 AAA-----ACTTTAATACATTTTGTATCTATATAGATCTATTAAGTTTCAATTTGTA 1326
Db 358 ArgLeuSerLysGlnLeuIleThrLeuLeuProGlyGlu-----PheIleThrHisLeuSer 376
Qy 1327 ACTGATAGACAAGTAACCTCTACTCTCCCTTTTCTTAACATATACTTTTCAATTAATCAA 1386
Db 377 IleAenArgGlyPheGlnThrIleAlaGlyIleAenLysLeuTyrrSerLeuIleGlnLys 396
Qy 1387 ATTGAATCTTTATTTAAATTAATTCACCTAGTAAATTAATTAACATATTTACGCTGGGGGAAT 1446
Db 397 Ile-----ValPheThrThrPheLysAenAspAenGluTyrrGlnLysAenPheAen 413

Qy 1447 TTATCTAATGAT-----AAAAAACCACTGATTTTCAATTTTCTCTGTAATAAAGAC 1497
Db 414 ValAenAenGlnAenGluProGlnGluThrThrAenTyrr----- 426
Qy 1498 TGTAAACCAATTTAATTAATTTCAAAATTTGTTTCAACAGCTATAATAGT-----TATAGTCAAT 1551
Db 427 -----ProAenAspTyrrGlyGlySerAenSerGlnLysPheLysHis 440
Qy 1552 ATTTTATCCCAAGTTTCTTTTATTTAATTTATTTCTTATATAATTTGGATTAGCGCTAATATA 1611
Db 441 AsnLeuSerHisPheProLeuIleIleHisGlnValGluPheAlaGluTyrrPheHisSer 460
Qy 1612 TTATATACAGTGTAGTATGAGACACACAGTAGTGTGTATAGAAAATAATGCAATATCA 1671
Db 461 IlePhe-----AlaLeuGlyTyrrThrHisAenSerValAenSerGlnAenLeuIleSer 478
Qy 1672 GATAAATAATTAATCAATGATCCAGCAATCAAGGTAAACAGTCTTTGTATACAACTCTAAG 1731
Db 479 GluSerValSerThrGlnIleProLeuValLysAlaTyrrGluValThrThrAenSer--- 497
Qy 1732 GTAATTGAGGACCTGCTCATACAGGAGAACTTGGTTTATTTTATTTTACAAAGTCAGGGCGT 1791
Db 498 ValIleArgGlyProGlyPheThrGlyGlyAspLeuIleGluLeuArgAsp-----Lys 515
Qy 1792 TTAGAGATTACATGTGAACCTCTTAATTTCTACACAACTCTTATTTATTTAGCTTCGATAC 1851
Db 516 CysSerIleLysCysLysAla---SerSerLeuLysLysTyrrAlaIleSerLeuPheTyrr 534
Qy 1852 GCTCAAAATGCTGCGAAATACCTCTTCTTAATATATCTTTTACAAATACCAAGGAGTAATA 1911
Db 535 AlaAlaAenAenAlaIleAlaValSerIleAspValGlyAspSerGlyAlaGlyValLeu 554
Qy 1912 GGAATACCCTCAACGACTCAACAACTTTTCTTCTGTACAAATTTATAATTAAT 1965
Db 555 -----LeuGlnProThrPheSerArgLysGlyAenAenAenPheThr 568
Qy 1966 -----TTCAATACGAGATTTTGGTATTTTCCAAATTTTCCAAAGTACATACATTA 2016
Db 569 IleGlnAspLeuAenTyrrLysAspPheGlnTyrrHisThrLeuLeuValAspIleGluLeu 588
Qy 2017 CTTTAAATCGAAACATACCATTTATATTTAATCTGTCAGAT-----GTATCAAAATCA 2070
Db 589 ProGluSerGluGluIleHisIleHisLeuLysArgGluAspAspTyrrGluGluGlyVal 608
Qy 2071 ATTTTATCATTTGATAAATTTGAATTTATACCAATTTACTTCTCTGTAGCCAAAATAGA 2130
Db 609 IleLeuLeuIleAspLysLeuGluPheLysProIleAspGluAenTyrr-----Thr 625
Qy 2131 GAAAAACAAAAATTAGAACTATCCAAACAAAAATAATACATTTTTCACAAATCATACA 2190
Db 626 AenGluMetAenLeuGluLysAlaLysLysAlaValAenValLeuPheIleAenAlaThr 645
Qy 2191 AAAAATCTTTAAATATAGAACCCCAAACTATGATATTGAT 2232
Db 646 ---AenAlaLeuLysMetAspValThrAspTyrrHisIleAsp 658

RESULT 4

C28AA BACTF STANDARD; PRT; 1109 AA.
ID C28AA BACTF AC Q9X682;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Peptidicidal crystal protein cry28AA (insecticidal delta-endotoxin
DE CryXXVIIIa) (Crystalline entomocidal protoxin) (126 kDa crystal
DE protein).
GN Name=cry28AA; Synonyms=cryXXVIIIa(a);
OS Bacillus thuringiensis subsp. finitimus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=29337;
RN [1]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN-VKPM B-1161;
 RX MEDLINE=99330166; PubMed=10403372; DOI=10.1016/S0014-5793(99)00650-X;
 RA Wojciechowska J.A., Lewitin E., Revina L.P., Zalunin I.A.,
 RA Chestukhina G.G.;
 RT "Two novel delta-endotoxin gene families cry26 and cry28 from *Bacillus*
 RT *thuringiensis* ssp. *finitimus*";
 RL PERS Lett. 43:46-48(1999).
 CC -1- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
 CC epithelial cells of insects.
 CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during
 CC sporulation and is accumulated both as an inclusion and as part of
 CC the spore coat.
 CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-
 CC terminus.
 CC -1- SIMILARITY: Belongs to the delta endotoxin family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 DR EMBL; AF132928; AAD24189.1; -, Genomic_DNA.
 DR HSP; O06117; IJ16.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR Pfam; PF03944; Endotoxin_C; 1.
 DR Pfam; PF00555; Endotoxin_M; 1.
 DR Pfam; PF03945; Endotoxin_N; 1.
 DR Sporulation; Toxin.
 KW SEQUENCE 1109 AA; 125714 MW; 10C80705508F5CDA CRC64;
 SQ
 Alignment Scores:
 Pred. No.: 1,36e-52 Length: 1109
 Score: 901.00 Matches: 240
 Percent Similarity: 49.23% Conservative: 106
 Best Local Similarity: 34.19% Mismatches: 242
 Query Match: 22.87% Indels: 114
 DB: 1 Gaps: 27
 US-10-782-570-1 (1-2235) x C28AA_BACTP (1-1109)
 QY 199 AGTCGTGATACAAATGCTGCTAGTACGAGTACTATGTATCGGTACTCTGTAGCC 258
 DB 28 SerSerAspThrValAlaValValSerAlaGlyIleValValGlyThrIleLeuThr 47
 QY 259 GGTATAGGTGGCTCAGTCTCTATATCCGACCGATAGGAATAATAGGTGCTATAATA 318
 DB 48 -----AlaPheAlaSerPheValAsnPro-----GlyValValLeuIle 60
 QY 319 TCTTTGGTACCCTAATCACTGTCTTTTGGCCCGGGGAGAACAGAC---AAACAGTA 375
 DB 61 SerPheGlyThrLeuAlaProValLeuTrpProAspProGluGluAspProLysIle 80
 QY 376 TGGACACAAATTTATTAATGGGAAATTTTGTGTATACACCGTTTAAACAGAACATA 435
 DB 81 TrpSerGlnPheMetLysGlyGluAspLeuLeuAsnGlnThrIleSerThrAlaVal 100
 QY 436 AAACAGCTAAAGTTACAACTTTAGACGATTTAGACAAATATTACAAAGCTATAATACA 495
 DB 101 LysGluIleAlaLeuAlaHisLeuAsnGlyPheLysAspValLeuThrTyTrpGluArg 120
 QY 496 GCATTAGATGATGGAGAAATTTAAAGAGACTACAAAGCTCTGGATTACCAACCATCATCA 555
 DB 121 AlaPheAsnAspTrpLysArg-----AsnProSerAla 131
 QY 556 GCATTACAAACAGCTGCTGACTCTTAAATATACGATTTGAGATGTTTCAACATGATTTT 615
 DB 132 -----AsnThrAlaArgLeuValSerGlnArgPheGluAsnAlaHisPheAsn 148
 QY 616 ATTCGAGAAATACCTGGTTTCCAACTTGAACCTTATAAACCGCTATTACTACTATTAT 675

Db 149 ValSerAsnMetProGlnLeuLeuLeuProThrTyAspThrLeuLeuLeuSerCysTyr 168
 QY 676 GCGCAAGCTGCTAATTTTAAATTTATTACAACAGGTGCTGAATTTGGCTGATGAA 735
 Db 169 ThrGluAlaAlaAsnLeuHisLeuAsnLeuHisGlnGlyValGlnPheAlaAspGln 188
 QY 736 TGGATCCAGATATACATCTCTCCAAATTGAACCTAATGCTGGAACATCAGATGACTAT 795
 Db 189 TrpAsnAlaAspGlnProHisSerProMetLeuLysSerSerGlyThr-----Tyr 205
 QY 796 TATAAATCTTTAAAGAAATATACCTAAATATAGTAACCTATTCTGCAATACCTATAGA 855
 Db 206 TyrAspGlnLeuLeuValTyIleGluLysTyIleAsnTyIleAsnTyIleHis 225
 QY 856 GAAGGACTAAATAAATTCGAAACGAACCTAATATAGATGGAGTATATTAATGATAT 915
 Db 226 LysGlyLeuAsnHisLeuLysGluSerGluLysIleThrTrpAspAlaTyAsnThrTyr 245
 QY 916 CGAAGATATATGACTATTACTGTATAGACTACTATCGCTCAATTTCTTTTATGATATA 975
 Db 246 ArgArgGluMetThrLeuIleValLeuAspLeuValAlaThrPheProPheTyrAspIle 265
 QY 976 AAGAGATACAAAGATTCAATAGGAAGAATAGGTGGCAATATAAAGCTGAACCTTACAAGAA 1035
 Db 266 ArgArgPhePro-----ArgGlyValGluLeuLeuLeuLeuThrArgGlu 279
 QY 1036 ATTATACAATGAAATTAATTTTGCAGCTTACTTACCTTGAATTTCAACCAATCTC 1095
 Db 280 ValTyThrSer-----LeuAspHisLeuThrArgProGly--- 292
 QY 1096 GCTATAATGGAATATAATTTAACACGTTTACGGCTTAGATATATTTTATGATGAA 1155
 Db 293 -----LeuPheThrTrpLeuSerAsp 299
 QY 1156 CTTATATTTTATACAAAAAATGAAACGTACGGGAATCGTTTAGTTGCTATTGCGAATCGT 1215
 Db 300 IleGluLeuTyThrGluSerValAlaGluGlyAspTyIleLeuSerGlyIle----- 316
 QY 1216 AATGATCTACTATGCTACGACAGGAACTGAAAT-----ATATATGGA 1260
 Db 317 ---ArgGluSerLysTyIleThrGlyAsnGlnPhePheThrMetLysAsnIleTyGly 335
 QY 1261 GAAAGACAGGTCCACCCACACACAAA-----ACTTAATACCAATTT 1302
 Db 336 Asn-----ThrAsnArgLeuSerLysGlnLeuIleThrLeuLeuProGly 350
 QY 1303 GAATCCTATAAAGTTTCAATTTGTAACCTGATAGACAAAGTAACCTCTACTCTCCCTTTTCC 1362
 Db 351 Glu---PheMetThrHisLeuSerIleAsnArgProPheGlnThrIleAlaGlyIleAsn 369
 QY 1363 AACATATCTTTACAATTAATCAAAATGAACTTTTATTAATAATTAATCACTAGTAATAAA 1422
 Db 370 LysLeuTyIleSerLeuIleGlnLysIle-----ValPheThrThrPheLysAsnAsp 386
 QY 1423 TTAACATATTCAGCTGGGGGAATTTATCTAATGAT-----AAAAAACCACTGAT 1473
 Db 387 AsnGluTyIleGlnLysAsnPheAsnValAsnAsnGlnAsnGluProGlnGluThrAsn 406
 QY 1474 TTTCAATTTCTGTAAAAAAGACTGTAAACCAATTTAATCAAAATTTGTTTACCAGC 1533
 Db 407 Tyr-----ProAsnAspTyIleGly 413
 QY 1534 TATAATAGT-----TATAGTCATATTTATCCAGATTTTCTTTTATTAATTTATTCCTAT 1587
 Db 414 SerAsnSerGlnLysPheLysHisAsnLeuSerHisPheProLeuIleHisLysLeu 433
 QY 1588 AAATTTGGATTAGCGCTAAATATATATATACAGTTCATTCAGTACACACAGTAGT 1647
 Db 434 GluPheAlaGluTyIlePheHisSerIlePhe-----AlaLeuGlyTyIleHisAsnSer 451
 QY 1648 GTTAATGAAATATGCAATATATCAGATAATAAATTAATTAACAATGATCCAGCAATCAAGGT 1707

Db 452 ValAsnSerGlnAsnLeuIleSerGluSerValSerThrGlnIleProLeuValLysAla 471
Qy 1708 AACAGCTCTTGATACAACTTAAGCTTAATGAGGAGCTGTGTCATACAGGAGGAACTTG 1767
Db 472 TyrGluVal---ThrAsnAsnSerValIleArgGlyProGlyPheThrGlyGlyAspLeu 490
Qy 1768 GTTATTATTACAAAGTCAAGGGCTTTAGAGTATCATGTAGAACTCTTAATCTACACAA 1827
Db 491 IleGluLeuArgAsp-----LysCysSerIleLysCysLysAla---SerSerLeuLys 507
Qy 1828 TCTTATTATCATGATCTGATACCTGATACCTGATACCTGATACCTGATACCTGATACCT 1887
Db 508 LysTyrAlaIleSerLeuPheTyrAlaAlaAsnAsnAlaIleAlaValSerIleAspLeu 527
Qy 1888 TCTCTTACATACACGAGGATATAGATATACCATCTCAACGACTCAACACACATTTTCT 1947
Db 528 GlyAspSerGlyAlaGlyValLeu-----LeuGlnProThrPheSer 541
Qy 1948 GGTACAAATTAATAAT-----TTACAATACGAGATTTTGGGTATTTTC 1992
Db 542 ArgLysGlyAsnAsnAsnPheThrIleGlnAspLeuAsnTyrLysAspPheGlnTyrHis 561
Qy 1993 CAATTTCCAGTACGATACATACCTTTAAATCGAAACATACCATTTATATTTAATCGT 2052
Db 562 ThrLeuLeuValAspIleGluLeuProGluSerGluGluIleHisIleHisLeuLysArg 581
Qy 2053 GCGAT-----GTATCAATTCATTTTATCATGTATGATTAATTAATTTATACCAAT 2106
Db 582 GluAspAspTyrGluGluGlyValIleLeuLeuIleAspLysLeuGluPheLysProIle 601
Qy 2107 ACTTCTCTGTACGCAAAATAGAGAAACAAATAATAGAACTATCCAAACAAATAA 2166
Db 602 AspGluAsnTyr-----ThrAsnGluMetAsnLeuGluLysAlaLysLysAlaVal 618
Qy 2167 ATATCATTTTTCACAAATCATACAAATAATCTTTAAATATATAGAGCCCAAACTATGAT 2226
Db 619 AsnValLeuPheIleAsnAlaThr---AsnAlaLeuLysMetAspValThrAspTyrHis 637
Qy 2227 ATGAT 2232
Db 638 IleAsp 639

RESULT 5

ClOAA_BACTI STANDARD; PRT; 675 AA.
AC P09662;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Pesticidal crystal protein cry10Aa (Insecticidal delta-endotoxin
DE CryXA(a)) (Crystalline entomocidal protoxin) (78 kDa crystal protein).
GN Name=cry10Aa; Synonyms=cryIVc, cryXA(a);
OS Bacillus thuringiensis subsp. israelensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1430;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=ONR60A;
RX MEDLINE=86223796; PubMed=3011746;
RA Thorne L., Garduno F., Thompson T., Decker D., Zounes M., Wild M.,
RA Walfield A.M., Pollock T.J.;
RT "Structural similarity between the lepidoptera- and diptera-specific
RT insecticidal endotoxin genes of Bacillus thuringiensis subsp.
RT 'kurstaki' and 'israelensis'";
RL J. Bacteriol. 166:801-811(1986).
CC -!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut
CC epithelial cells of mosquitos. Active on Aedes aegypti.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.

CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL; M12662; AAA22614.1; -, Genomic_DNA.

DR PIR; B29838; B29838.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR Pfam; PF03944; Endotoxin C; 1.
DR Pfam; PF00555; Endotoxin M; 1.
DR Pfam; PF03945; Endotoxin N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 675 AA; 77761 MW; 2A70011BEA7985F5 CRC64;

Alignment Scores:

Pred. No.: 24e-52 Length: 675
Score: 897.00 Matches: 251
Percent Similarity: 47.96% Conservative: 114
Best Local Similarity: 32.98% Mismatches: 268
Query Match: 22.77% Indels: 128
DB: 1 Gaps: 32

US-10-782-570-1 (1-2235) x ClOAA_BACTI (1-675)

Qy 13 AATATATATGATATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 72
Db 6 AsnLysAsnGluTyrGluIlePheAsnAlaProSerAsnGlyPheSerLysSerAsn 25
Qy 73 ATTGATCATTTAGTATACCTTACACAAATATCAAAATCAACATCAACATCAACATCAACAT 132
Db 26 -----TyrSerArgTyrProLeuAlaAsnLysProAsnGlnProLeuLysAsnThrAsn 43
Qy 133 TACAAGAGTGGCTCAATATGTCTCAAGGGAATACACAAATATGGTGATATTCGAGACA 192
Db 44 TyrLysAspTrpLeuAsnValCysGlnAspGlnGlnTyrGlyAsnAsnAlaGlyAsn 63
Qy 193 TTTGCTAGTGTGATACAAATTTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 252
Db 64 PheAlaSerSerGluThrIleValGlyValSerAlaGlyIleIleValValGlyThrMet 83
Qy 253 TTAGCCGTATAGTGGGCTCACTCTATATCCGACCGATAGGATATAGTGTGTATA 312
Db 84 LeuGly-----AlaPheAlaPro-----ValLeuAlaAlaGly 95
Qy 313 ATAATATCTTTTGTACCTTAATCACTGTCTTTTGGCCGCGGAGAACACAGACAAACAA 372
Db 96 IleIleSerPheGlyThrLeuLeuProIlePheTrp-----GlnGlySerAspProAlaAsn 114
Qy 373 GTATGGACACAAATTTATTAAATGGGAGAAATTTTGTGTATACACCGTTAACAGAA---- 429
Db 115 ValTrpGlnAspLeuLeuAsnIleGly-----GlyArgProIleGlnGluIle 130
Qy 430 -----AGCATAAACACGTAAAGTTACAAACTTTAGAGAGGATTTAGACAAATATATACA 483
Db 131 AspLysAsnIleIleAsnValLeuThrSerIleValThrProIleLysAsnGlnLeuAsp 150
Qy 484 AGCTATATACAGCATTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 543
Db 151 LysTyrGlnGluPhePheAspLysTrpGluProAlaArg----- 163
Qy 544 CCACCATCATCAGCATTAACAAACGCTGCTTGTACTCTTAAATACGATTTGAGATGTT 603
Db 164 -----ThrHisAlaAsnAlaLysAlaValHisAspLeuPheThrThrLeuGluProIle 181
Qy 604 CACAAT-----GATTTTATTCGAGAAATACCTGGTTTCCAACTTGAACCTTATAAA 654
Db 182 IleAspLysAspLeuAspMetLeuLysAsnAsnAlaSerTyrArgIleProThr----- 199

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QY 655 ACGCTATTACTACCTATTATGCGCAAGCTGCTAATTTTCTTAAATTTATTACACAA 714
Db 200 -----LeuProAlaTyrAlaGlnIleAlaThrTrpHisLeuAsnLeuLeuLysHis 216
QY 715 GGTGCTGAATGGCTGCGAATGGAATGCGAGATATACATCTCTTCAAAATTTGAACCTAAT 774
Db 217 AlaAlaThrTyrTyrAsnIleTrp-----LeuGlnAsnGlnGlyIleAsnProSer 233
QY 775 GGTGGAACATCAGACTATTATATAA---CTTTTAAAGAAATATATACCTAAATATAGT 831
Db 234 ThrPheAsnSerSerAsnTyrTyrGlnGlyTyrLeuLysArgLysIleGlnGluTyrThr 253
QY 832 AACTATTGTCGAAATACCTATAGAGAGAGCTTAATAACTTCGAAACGACCTAATATG 891
Db 254 AspTyrCyHisIleGlnThrTyrAsnAlaGlyLeuThrMetIleArgThrAsnThrAsnAla 273
QY 892 AGATGGAGTATATTAATGATTATCGAAGATATATGACTATTACTGTATTAGACTATATC 951
Db 274 ThrTrpAsnMetTyrAsnThrTyrArgLeuGluMetThrLeuThrValLeuAspLeuIle 293
QY 952 GCTCAATTTCTTTTATGATATAAGAGATACAAAGATTCATAGGAAATAGGTGGC 1011
Db 294 AlaIlePheProAsnTyrAspProGluLysTyrProIle-----Gly 307
QY 1012 ATTAAGACTGAACTTACAGAGAAATTTATACACTGAAATTAATTTTGACCGTCTTACT 1071
Db 308 ValLysSerGluLeuIleArgGluValTyr---ThrAsnValAsnSerAspThrPheArg 326
QY 1072 TACCTTGAAATTCACCCCAATCTCGCTATATGGAATATAATTTAAACACGTTTCAGGGCTT 1131
Db 327 -----ThrIleThrGluLeuGluAsnGlyLeuThrArgAsnPro--- 339
QY 1132 AGATTATTTTCATTTTATAGTGAATCTATATTTTATACAAAAAT- 1176
Db 340 ThrLeuPheThrTrpIleAsnGlnGlyArgPheTyrThrArgAsnSerArgAspIleLeu 359
QY 1177 GAAACGTATC-----CGGAATCGTTTGTAGTTGGTATTGCGAATCGTAAAT 1218
Db 360 AspProTyrAspIlePheSerPheThrGlyAsnGlnMetAla----- 373
QY 1219 AGATCTACTTGTCTACGACAGGAAGTCAAAATTTATATATGAGAAAGAACAGGT----- 1272
Db 374 ---PheThrHisThrAsnAspArgAsnIleIleTrpGlyAlaValHisGlyAsnIle 392
QY 1273 ---CCACCCACACAAAACTTTAATACATTTGAAATCCTAT-----AAAGTT 1317
Db 393 IleSerGlnAspThrSerLysValPheProPheTyrArgAsnLysProIleAspLysVal 412
QY 1318 TCATTTGTAAGTATGATAGACAAGTAAGTCTCTACTCCCTTTTCTTCAATATATCTTTACA 1377
Db 413 GluIleValArgHisArgGlu-----TyrSerAsp 422
QY 1378 ATTAATCAATGAATGAACTTTATTTAAATTAATTCACCTAGTAAATTAACATATTCAGCT 1437
Db 423 IleIleTyrGluMetIlePhePheSerAsnSer---SerGluValPheArgTyrSerSer 441
QY 1438 GGGGGGAATTTATCTAATGATATAAAAAACAACACTGATTTTCAATTTTCCCTGTATAAAAAAGAC 1497
Db 442 AsnSerThrIleGluAsnAsnTyrLysArgThrAspSerTyrMetIleProLysGlnThr 461
QY 1498 TGTAAACCAATTAATTCAAATTTGTTTACCAAGCTATAATAGTATTAGTCATATTTTA 1557
Db 462 TrpLys-----AsnGluGluTyrGlyHisThrLeu 471
QY 1558 TCCAGATTTTCTTTTATTAATTTATCTCTATAAAATTTGGATTAGCGCTAAATATATATAT 1617
Db 472 SerTyrIleLysThrAspAsnTyrIlePheSerVal-----ValArgLysArg 488
QY 1618 ACAGGTGCATTAGGATGACACACAGTAGTGTATTAAGAAATAATGCAATATCAGATAAA 1677
Db 489 ArgValAlaPheSerTrpThrHisThrSerValAspPheGlnAsnThrIleAspLeuAsp 508
QY 1678 ATAATTACATGATCCCGAGCAATCAAGGTAAACAGTCTTGTGTATACAAACTCTAAGCTAAT 1737

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Db 509 AsnIleThrGlnIleHisAlaLeuLysAlaLeuLysValSerSerAspSerLysIleVal 528
QY 1738 CAAGACCTGCTCATACAGAGAAAGCTGTTGTTTATTTACAAAGTCAAGGCGGTTTAGAG 1797
Db 529 LysGlyProGlyHisThrGlyGlyAspLeuValIleLeuLysAspSer-----MetAsp 546
QY 1798 ATTACATGTAGA---ACTCTTAATTTCTACACAATCTTATTACATAGACTTCGATCGCT 1854
Db 547 PheArgValArgPheLeuLysAsnValSerArgGlnTyrGlnValArgIleArgTyrAla 566
QY 1855 ACAAATCGTCTGGAATACTCTCTCTAATATATCTCTTACAAATACCAAGGAGTAATAGGA 1914
Db 567 ThrAsnAla-----ProLysThrThrValPheLeuThrGlyIleAspThr 581
QY 1915 ATACCACTCAACGACTCAACACACTTTTCTGGTACAAATATAAT-----AATTTA 1968
Db 582 IleSerValGlu---LeuProSerThrThrSerArgGlnAsnProAsnAlaThrAspLeu 600
QY 1969 CAATACGAGGATTTGGGTATTTCCAAATTTCCAAAGTACAGTA----- 2010
Db 601 ThrTyrAlaAspPheGlyTyrValThrPheProArgThrValProAsnLysThrPheGlu 620
QY 2011 -----ACATTACCTTTAAATCGAAACATACCATTTATATTTAATCGTGCAGATGTA 2061
Db 621 GlyGluAspThrLeuLeuMetThr-----LeuTyrGlyThrProAsnHis 635
QY 2062 TCAAAATTCAAATTTTAATCATTGATGATAAAATTTGAATTTATATACCAATTTCTCTGTACGC 2121
Db 636 SerTyrAsnIle---TyrIleAspLysIleGluPheIleProIleThrGlnSerValLeu 654
QY 2122 CAAAATAGAGAAACAAAAAATTAGAACTATCCAAACAAAAATAAATACATTTTCCACA 2181
Db 655 AspTyrThrGluLysGlnAsnIleGluLysThrGlnLysIleValAsnAspLeuPheVal 674
QY 2182 AAT 2184
Db 675 Asn 675

RESULT 6
Q8KNV2_BACTI
ID Q8KNV2_BACTI PRELIMINARY; PRT; 675 AA.
AC Q8KNV2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Peptidicidal crystal protein cry10AA.
GN Name=cry10AA; Synonyms=cryIVC, cryXA(A), pBt047;
OS Bacillus thuringiensis (subsp. israelensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1430;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22235415; PubMed=12324359;
RX DOI=10.1128/AEM.68.10.5082-5095.2002;
RA Berry C., O'Neil S., Ben-Dov E., Jones A.F., Murphy L., Quail M.A.,
RA Harris D., Zaritsky A., Parkhill J.;
RT "Complete sequence and organisation of pBtoxis, the toxin-coding
RT plasmid of Bacillus thuringiensis subsp. israelensis.";
RL Appl. Environ. Microbiol. 68:5082-5095(2002).
DR EMBL; AL731825; CAD30098.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.

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SQ SEQUENCE 675 AA; 77759 MW; 4EB0851AA0372FF1 CRC64;

Alignment Scores:

Pred. No.: 2.4e-52 Length: 675
 Score: 897.00 Matches: 251
 Percent Similarity: 47.96% Conservative: 114
 Best Local Similarity: 32.98% Mismatches: 268
 Query Match: 22.77% Indels: 128
 DB: 2 Gaps: 32

US-10-782-570-1 (1-2235) x 09KNV2_BACTI (1-675)

QY 13 AATAATAATGAATATGAGATTCATTCAGATTCAGAAAGATTTATCTTATCTTCTTCAACAGAAAT 72
 DB 6 AsnLysAsnGluTyrGluIlePheAsnAlaProSerAsnGlyPheSerLysSerAsnAsn 25
 QY 73 ATTGATCAATTCAGATACCTTACACAAATATCAATCAACCAATTCACCAATTCACCAAT 132
 DB 26 -----TyrSerArgTyrProLeuAlaAsnLysProAsnGlnProLeuLysAsnThrAsn 43
 QY 133 TACAAGAGTGGCTCAATATGCTCAAGGGATATACACAAATATGCTGATATTCGAGACA 192
 DB 44 TyrLysAspTrpLeuAsnValCysGlnAspAsnGlnTyrGlyAsnAlaGlyAsn 63
 QY 193 TTTCGTAGTCTGATACAAATGCTGCAGTTAGTGCAGGTACTATTGTATCCGTTACTCTG 252
 DB 64 PheAlaSerSerGluThrIleValGlyValSerAlaGlyIleIleValValGlyThrMet 83
 QY 253 TTAGCCGGTATAGTGGGCTCACTTCTATATCCGACCGCATAGGATATAGTCTATATA 312
 DB 84 LeuGly-----AlaPheAlaPro-----ValLeuAlaAlaGly 95
 QY 313 ATAATATCTTTGGTACCTAATCACTGCTTTTGGCCGGGGAGAACACAGACAAACA 372
 DB 96 IleIleSerPheGlyThrLeuLeuProIlePheTrp-----GlnGlySerAspProAlaAsn 114
 QY 373 GTATGGACACAAATTTATTAATAATGGAGAAATTTTGTGTATACACCGTTAACAGAA--- 429
 DB 115 ValTrpGlnAspLeuLeuAsnIleGly-----GlyArgProIleGlnGluIle 130
 QY 430 -----AGCATATAACAGCTAAAGTTACAACTTTAGAGAGGATTTAGACAAATATACAA 483
 DB 131 AspLysAsnIleIleAsnValLeuThrSerIleValThrProIleLysAsnGlnLeuAsp 150
 QY 484 AGCTATAATACGATTAATGATGATGGAGAAATTTAAAGACTACAGCTCTCGATTA 543
 DB 151 LysTyrGlnGluPhePheAspLysTrpGluProAlaArg----- 163
 QY 544 CCACCATCATCAGCATTAACAAGCTGCTTGAAGCTCTTAAATACGATTTGAGAAATGTT 603
 DB 164 -----ThrIleAlaAsnAlaLysAlaValHisAspLeuPheThrThrLeuGluProIle 181
 QY 604 CACAAT-----GATTTTATTCGAGAAATACCTGGTTTCCAACTTGAACCTTATAAA 654
 DB 182 IleAspLysAspLeuAspMetLeuLysAsnAsnAlaSerTyrArgIleProThr----- 199
 QY 655 AGCTATTACTACTATTATTCGCGAGCTGCTAATTTTCATTTTAAATTTATACACAA 714
 DB 200 -----LeuProAlaTyrAlaGlnIleAlaThrTrpHisLeuAsnLeuLeuLysHis 216
 QY 715 GGTGCTGAATTCGGTGAATGGAATGCAGATATATACATCTTCCAAATTCGAACCTAAT 774
 DB 217 AlaIleThrTyrTyrAsnIleTrp-----LeuGlnAsnGlnGlyIleAsnProSer 233
 QY 775 GCTGGAACATCAGATCTATTATATAA-----CTTTTAAAGAAATAATATACCTAATATAGT 831
 DB 234 ThrPheAsnSerSerAsnTyrTrpGlnGlyTyrLeuLysArgLysIleGlnGluTyrThr 253
 QY 832 AACTATTGCGAAATACCTATAGAGAGGACTAATAAATCTTCGAAACGAACTAATATG 891
 DB 254 AspTyrCysIleGlnThrThrAsnAlaGlyLeuThrMetIleArgThrAsnThrAsnAla 273
 QY 892 AGATGGAGTATATTTAATGATTTATCGAAGATATATAGCTATTACTGTATAGATATATC 951

DB 274 ThrTrpAsnMetTyrAsnThrTyrArgLeuGluMetThrLeuThrValLeuAspLeuIle 293
 QY 952 GCTCAATTTTCTTTTATGATATAAAGAGATACAAAGATTCAATAGGAAGATAGGTGCG 1011
 DB 294 AlaIlePheProAsnTyrAspProGluLysTyrProIle-----Gly 307
 QY 1012 ATTAAACTGAACCTTACAGAGAAATTTATACAACTGAAATATAATTTTTCACCGCTCTTACT 1071
 DB 308 ValLysSerGluLeuIleArgGluValTyr---ThrAsnValAsnSerAspPheArg 326
 QY 1072 TACCTTGAAATTCACCAATCTCGCTATATGAATATATAATTTAAACAGTTCAGGGCTT 1131
 DB 327 -----ThrIleThrGluLeuGluAsnGlyLeuThrArgAsnPro--- 339
 QY 1132 AGATTATTTTCATTTTAGATGAACCTTATATTTTATATACAAAAT----- 1176
 DB 340 ThrLeuPheThrTrpIleAsnGlnGlyArgPheTyrThrArgAsnSerArgAspIleLeu 359
 QY 1177 GAAACGTAC-----GGGAATCGTTTAGTTGGTATTGCGAATCGTAAT 1218
 DB 360 AspProTyrAspIlePheSerPheThrGlyAsnGlnMetAla----- 373
 QY 1219 AGATCTACTATGCTACGACAGAACTGAAATTTATATATGAGAAAGAACAGGT----- 1272
 DB 374 ---PheThrHisThrAsnAspAspArgAsnIleIleTrpGlyAlaValHisGlyAsnIle 392
 QY 1273 ---CCACCCACACAAACCTTTAATACCATTTGNAATCTAT-----AAAGTT 1317
 DB 393 IleSerGlnAspThrSerLysValPheProPheTyrArgAsnLysProIleAspLysVal 412
 QY 1318 TCAATTGTAACTGATAGACAAAGTAACCTCTACTCTCCCTTTTCTTAAACATATCTTTACA 1377
 DB 413 GluIleValArgHisArgGlu-----TyrSerAsp 422
 QY 1378 ATTAATCAAAATTGAATTTTATTAATAATTAATCACTAGTATAATAATTAATCAATATTCAGT 1437
 DB 423 IleIleTyrGluMetIlePhePheSerAsnSer---SerGluValPheArgTyrSerSer 441
 QY 1438 GGGGGGAATTTATCTAATGATAAATAAACAACACTGATTTTCAATTTCTGTATAAAGAAC 1497
 DB 442 AsnSerThrIleGluAsnAsnTyrLysArgThrAspSerTyrMetIleProLysGlnThr 461
 QY 1498 TGTAAACCAATTTATTAATCCAAATTTGTTTACCAAGCTATAATAGTATATAGTATATTTA 1557
 DB 462 TrpLys-----AsnLysGluTyrGlyHisThrLeu 471
 QY 1558 TCCCAAGTTTCTTTATTTATTTATTTCTTATAAATTTGGATTAGCCCTAAATATATATAT 1617
 DB 472 SerTyrIleLysThrAspAsnTyrIlePheSerVal-----ValArgGluArgArg 488
 QY 1618 ACAGGTGCATTTAGGATGGACACACAGTAGTGTATAGATAATAATAGCAATATACATATAA 1677
 DB 489 ArgValAlaPheSerTrpThrHisThrSerValAspPheGlnAsnThrIleAspLeuAsp 508
 QY 1678 ATAATTACAATGATCCAGCAATCAAGGTAAACAGCTCTTGATACAACTCAAGGTAAAT 1737
 DB 509 AsnIleThrGlnIleHisAlaLeuLysAlaLeuLysValSerSerAspSerLysIleVal 528
 QY 1738 GAAGACCTGGTCTATACAGGAGAACTTGGTTTATTTTCAAGGTCAAGGGCTTTAGAG 1797
 DB 529 LysGlyProGlyHisThrGlyAspLeuValIleLeuLysAspSer-----MetAsp 546
 QY 1798 ATTACATGTAGA---ACTCCTAATTTCTACACATCTTATTAATCATTTAGCTTCGATACGCT 1854
 DB 547 PheArgValArgPheLeuLysAsnValSerArgGlnTyrGlnValArgIleArgTyrAla 566
 QY 1855 ACAATGGTGTGGAAATACTCTTCTAATATATCTTCTTACCAATACCAAGGTAAATAGGA 1914
 DB 567 ThrAsnAla-----ProLysThrThrValPheLeuThrGlyIleAspThr 581
 QY 1915 ATACCACCTCAACGACTCAACACACTTTTCTCGGTACAAATTAATAAT-----AATTTA 1968

Db	44	Tyr	Leu	Asp	Trp	Thr	Asn	Met	Cy	Ala	Ile	Asp	Asn	Asn	Leu	Leu	Val	Ser	Ile	Asn	Pro	Phe	63
Qy	187	GAG	ACA	CTT	TCT	AGT	GCT	GAT	ACA	CAAT	TGCT	GCA	GTAGT	TAGT	GCG	AGT	CTA	TGT	GAT	CCGGT		246	
Db	64																					83	
Qy	247	ACT	CTG	TAC	CGG	TAT	AGT	TGG	GCT	CAC	TTC	TAT	ATC	CGG	ACC	GAT	GAG	AAT	TA	AGGT		306	
Db	84																					103	
Qy	307	GCT	ATA	TAT	AAT	CTT	TGGT	TAC	CTCAAT	CAC	TGCT	TTT	GGCCG	CGCGG	AGAC	AAC	GAAG	C				366	
Db	104																					114	
Qy	367	AAA	ACG	TAT	TGG	ACAC	CAAT	TAT	TAA	ATG	GGG	GAA	AAAT	TTT	TGTT	GAT	CAC	CGT	TAA	CA		426	
Db	115																					134	
Qy	427	GAA	AGC	ATA	AAA	CAG	CTA	AAG	TTA	CAAA	CTTT	TAGA	AGG	ATTT	TAG	ACAA	CAAT	TATT	TAC	AAAGC		486	
Db	135																					154	
Qy	135	Gln	Arg	Val	Arg	Gln	Asp	Ala	Leu	Thr	Arg	Cys	Glu	Glu	Ser	Leu	Leu	Val	Asp	Ser	Val	154	

ACCA 546

155	PheGluAsnAlaPheThrPheTrpIleAsn-	-----Asn	165
547	CCATCATCAGCATTAACAACAAGCTGCGTCTTAAAAATACGATTGAGAAATGTTCCAC	606	
166	ProAsnSerThr-----AsnThrThrValArgGluArgPheGlnGluValAsn	182	
607	AATGATTTTATTCGAGAATACTCGTGTTCCTGAACTTATAAAACGCTATTACTTA	666	
183	GlyArgPheValGlySerMetalpPheArgAlaLysAsnTyrGluProIleLeuLeu	202	
667	CCTATTATTGCGCAAGCTGCTAATTTTCATTTAAATTTATTACAACAAGSTGCTGAATG	726	
203	SerThrTyrAlaGlnAlaAlaArgLeuHisLeuLeuHisLeuArgAspGlyIleThrTyr	232	
727	GCTGATGATGGAAATGCAGATATACATCTCTTCAAAATTGAACCTAATGCTGGAACATCA	786	
223	AlaGluIleTrpAsnLeuSerArgGlnGlyAspAspMet-----ProGly	237	
787	GATGACTATTATAAACTTTTAAAGAATAATACCTAAATATAGTAACTATTGTGCAAAT	846	
238	AspLeuLeuTyrIleGluPheAsnIleTyrCysAsnGluTyrIleGluHisCysIleLeu	257	
847	ACCTATAGAGAGGACTAAATAAACTTCGAAACGACCTAAATATGATGAGTGGACTATATTT	906	
258	TrpTyrAsnGluSerLeuLeuLeuLysSer---ValGlyAlaAsnTrpLeuGluTyr	276	
907	AATGATTTATCGAAGATATATGACTATTACTGTATTAGTACTATCGCTCAATTTCTTTT	966	

[illegible]


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QY 1612 TTATATACAGGTGCATTAGGATGACACACAGTAGTGTATATAGAAATAATGCAATATCA 1671
Db 464 -----TTPHrhlslylleValAspProhAsnGlnIleTyr 476
QY 1672 GATAAAATAATTACATGATCCCGCAATCAAGGTAAACAGTCTTGTATACAAACTTAAG 1731
Db 477 ThrAspAlaIleThrGlnValProAlaValLysSerAsnPheLeuAsnAlaThrAlaLys 496
QY 1732 GTAATTAGAGCACTGCTCATACAGGAGGAACCTGGTTTATTATTTACAAAGT----- 1782
Db 497 VallileysGlyProGlyHisThrGlyGlyAsnValAlaLeuThrSerAsnGlyThr 516
QY 1783 ---CAAGGGCTTTAGAGATTACATGTAGAACTCT-----AATTCTACACAATCT 1830
Db 517 LeuSerGlyArgMetGluGlnCysLysThrSerIlePheAsnAspProThrArgSer 536
QY 1831 TATTACATAGATCGTACGCTCAAAATCGTCTCGGAATATCTTCTCCTAATATATCT 1890
Db 537 TyrGlyLeuArgIleArgTyrAlaAlaAsnSerPro-----IleValLeuAsnValSer 554
QY 1991 CTTACAAATACAGGAGTAATAGGAATACCACCTCAAGCTCAACACACTTTTCTGGT 1950
Db 555 TyrValLeuGlnGlyValSerArgGlyThrThrIleSerThrGluSerThrPheSerArg 574
QY 1951 ACAAAATTAT-----ATAAATTACAATACGAGATTTTGGGTATTTCCAA---TTT 1998
Db 575 ProhAsnIleIleProThrAspLeuLysTyrGluGluPheArgTyrLysAspProPhe 594
QY 1999 CCAAGTACAGTAACATTTAACTTAAATCGAAAC-----ATACCATTTTATTTAATCGT 2052
Db 595 AspAlaIleValProMetArgLeuSerSerAsnGlnLeuIleThrIleAlaIleGlnPro 614
QY 2053 GCAGATGA---TCAATTCAATTTAATCATGTATGATAAAATGAATTTATACCAATACT 2109
Db 615 LeuAsnMetThrSerAsnAsnGlnValIleIleAspArgIleGluIleProIleThr 634
QY 2110 TCCTCTGTACGCCAAATPAGAGAAAACAAATAATTTAGAAACTATCCAAACAAATAAAT 2169
Db 635 GlnSerValLeuAspGluThrGluAsnGlnAsnLeuGluSerGluArgGluValValAsn 654
QY 2170 ACATTTTTCACAAATCATACAAAATACTTTAAATATAGAGCCACAACTATGATATT 2229
Db 655 AlaLeuPheThrAsnAspAlaLysAspAlaLeuAsnIleGlyThrThrAspTyrAspIle 674
QY 2230 GAT 2232
Db 675 Asp 675

RESULT 9
Q7AL72_BACTI
ID Q7AL72_BACTI PRELIMINARY; PRT; 1136 AA.
AC Q7AL72;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE Pesticidal crystal protein cry4BA.
GN Name=cry4BA; Synonyms=878, cryD2, cryIVB(A), IserH3, pBt038;
OS Bacillus thuringiensis (subsp. israelensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1430;
RN [1]
RX NUCLEOTIDE SEQUENCE.
RP MEDLINE=2235415; PubMed=12324359;
RX DOI=10.1128/ASM.68.10.5082-5095.2002;
RA Berry C., O'Neil S., Ben-Dov E., Jones A.F., Murphy L., Quail M.A.,
RA Harris D., Zaritsky A., Parthill J.,
RT "Complete sequence and organisation of pBtoxis, the toxin-coding
RT plasmid of Bacillus thuringiensis subsp. israelensis."
RL Appl. Environ. Microbiol. 68:5082-5095 (2002).
DR EMBL; AL731825; CAD30095.1; -; Genomic DNA.
SQ SEQUENCE 1136 AA; 127763 MW; 8AC4E8C26FE3E9B5 CRC64;
```

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Alignment Scores:
Pred. No.: 4,97e-47 Length: 1136
Score: 819.00 Matches: 246
Percent Similarity: 47.70% Conservative: 117
Best Local Similarity: 32.33% Mismatches: 268
Query Match: 20.79% Indels: 130
DB: 2 Gaps: 33

US-10-782-570-1 (1-2235) x Q7AL72_BACTI (1-1136)
QY 79 CATTCTAGATACCTCTTACACAAATAATCAACATTAACCAATTAACAAACACAAATTAACAA 138
Db 2 AsnSerGlyTyrProLeuAlaAsnAspLeuGlnGlySerMetLysAsnThrAsnTyrLys 21
QY 139 GAGTGGCTCAATATGCTCAAGGGAATACACAATATGTTGATATTTTCGAGACATTTGCT 198
Db 22 AspTrpLeuAlaMetCysGluAsnAsnGlnGlnTyrGlyValAsn-----Pro 37
QY 199 AGTCTCTGATACAAATGCTGCAGTTAGTGCAGGTACTATTGTATCCGGTACTCTCTGTAGCC 258
Db 38 AlaAlaIleAsnSerSerValSerThrAlaLeuLysValAlaGlyAlaIle----- 55
QY 259 GGTATAGGTGGCTCACTCTTATATCCGACCGATAGGAATAATAGTGTCTATTAATAATA 318
Db 56 -----LeuLysPheValAsnProProAlaGlyThrValLeuThrValLeu--- 70
QY 319 TCTTTTGGTACCTTAATCACTGCTTTTGGCCCGGGGA---GAACAGACAAACAGTA 375
Db 71 -----SerAlaValLeuProIleLeuTrpProThrAsnThrProThrProGluArgVal 88
QY 376 TGGACACAAATTTATAAATGGGAGAAATTTTGTCTGATACACCGTTTAAACAGAAAGCAT 435
Db 89 TrpAsnAspPheMetThrAsnThrGlyAsnLeuIleAspGlnThrValThrAlaTyrVal 108
QY 436 AAACAGCTAAAGTTACAAACTTTAGAGAGATTTAGACAAATATTAACAAAGCTATAATACA 495
Db 109 ArgThrAspAlaAsnAlaLysMetThrValValLysAspTyrLeuAspGlnTyrThrThr 128
QY 496 GCATTAGATGTTGGAGAAATTTAAAGACTACAAGCTCTCGGATTTACCAACCATCATCA 555
Db 129 LysPheAsnThrTrpLysArg-----GluProAsnAsnGln 140
QY 556 GCATTACACAAAGCTGCTTGAACCTTTAAATAACGATTTGAGAAATGTTCAACATGATTTT 615
Db 141 SerTyrArgThrAlaValIleThr-----GlnPhe---AsnLeuThrSerAlaLys 156
QY 616 ATTCGAGAAATACCTGGTTTC-----CAACTGAACTTATAAAACGCTATTACTACT 669
Db 157 LeuArgGluThrAlaValTyrPheSerAsnLeuValGlyTyrGluLeuLeuLeuPro 176
QY 670 ATTTATGGCAGCTGCTTAATTTTCAATTAAATTTATTAACAACAGGTGCTGAATGGCT 729
Db 177 IleTyrAlaGlnValAlaAsnPheAsnLeuLeuIleArgAspGlyLeuIleAsnAla 196
QY 730 GATCAATGGAATGCAGATATATACATCTCTTCAAAATTTGAACCTTAATGCTGGACATCAGT 789
Db 197 GlnGluTrpSer-----LeuAlaArgSerAlaGly-----Asp 207
QY 790 GACTATTATAAACTTTTAAAGAAATAATATACCTAAATATAGTAATCTATTGGCAATACC 849
Db 208 GlnLeuTyrAsnThrMetValGlnTyrThrLysGluTyrIleAlaHisSerIleThrTrp 227
QY 850 TATAGAGAGGACTAAATAAATCTTGAACCAACTAATATAGATGAGTATATTAAT 909
Db 228 TyrAsnLysGlyLeuAspValLeuArgAsnLysSerAsnGlnGlnTrpIleThrPheAsn 247
QY 910 GATTATCAAGATATATGACTATTACTGTATTAGTACTATCTCGCTCAATTTCTTTTAT 969
Db 248 AspTyrLysArgGluMetThrIleGlnValLeuAspIleLeuAlaLeuPheAlaSerTyr 267
QY 970 GATATAAGAGATAC---AAAGNTTCAATAGGAAGAATAAGTGGCATTTAAACTGAATT 1026
Db 268 AspProArgArgTyrProAlaAspLysIleAspAsnThrLysLeuSerLysThrGluPhe 287
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Qy	1027	ACAAGAGAAATTTATACAACTGAAATAAATTTTGACCGCTTACTTACCTTGAATCA	1086
Db	288	ThrArgGluIleTyThrAla-----LeuValGluSerProSerSer	301
Qy	1087	CCCAATCTCGCTATAATGAATATAATTTAAACAGCTTCAGGCGCTAGATATTTCATTT	1146
Db	302	LysSerIleAlaLeuGluAlaLeuThrArgAsp---ValHisLeuPheThrTrp	320
Qy	1147	TTAGATGAACCTTATATTTATACAAAATGAACGTHACGGAAAT	1191
Db	321	LeuLysArgValAspPheThrTrp---AsnThrIleTyGlnAspLeuArgPheLeuSer	339
Qy	1192	---CGTTAGTTGGTATGCGAATCGTAATAGATCTACTTATGCTACGACAGGAGTAA	1248
Db	340	AlaAsnLysIleGlyPheSerTyThrAsnSerSerAlaMetGlnGluSerGly-----	357
Qy	1249	ATTATATGAGAAAGAACAGAGCTCCACCCACAACAAAACCTTTAAATACCAATTC	1308
Db	358	---IleTyGlySerSerGlyPheGlySerAsnLeuThrHisGlnIleGlnLeuAsnSer	376
Qy	1309	-----TATAAGTTTCAATGTTACTGATAGACAAAGTAACCTCTACTCCCTTTTCCT	1362
Db	377	AsnValTyLysThrSerIle-----ThrAspThrSer-----	387
Qy	1363	AACATATACTTTACAAATTAATCAAAATTCGAATTTATTAATTAATTCACCTAGTAATA	1422
Db	388	-----SerProSerAsnArg	392
Qy	1423	TTAACA-----TATTACGCTGGGGGAATTTATCTAAT	1455
Db	393	ValThrLysMetAspPheTyLysIleAspGlyThrLeuAlaSerTyAsnSerAsnIle	412
Qy	1456	-----GATAAAACAACTGATTTTCAATTTCTCTGTAAACAAAGACTGT	1500
Db	413	ThrProThrProGluGlyLeuArgThrThrPheGlyPheSerThrAsnGluAsn---	431
Qy	1501	AAACCAATTAATTAATCAAAATTTGTTACCAAGCTATATAGTATAGTATATTTATCC	1560
Db	432	-----ThrProAsn-----GlnProThrValAsnAspTyThrHisIleLeuSer	446
Qy	1561	-----CAGTTTCTTTATTAATATAT---TCCTATAAAATTTGGATTAGCCCTAAATATA	1611
Db	447	TyrIleLysThrAspValIleAspTyAsnSerAsnArgValSerPheAla-----	463
Qy	1612	TTATATACAGTGCATTAGTAGGACACAGTAGTGTATAGTAATAATAGCAATATCA	1671
Db	464	-----TrpThrHisLysIleValAspProAsnAsnGlnIleTy	476
Qy	1672	GATAAAATTAATTAATGATCCAGCAATCAAGGTAACTCTTGATACAACTCTGAAG	1731
Db	477	ThrAspAlaIleThrGlnValProAlaValLysSerAsnPheLeuAsnAlaThrAlaLys	496
Qy	1732	GTAATTGAAGGACCTGGTCATACAGGAGAACTTGGTTATTTACAAAGT-----	1782
Db	497	ValIleLysGlyProGlyHisThrGlyAspLeuValAlaLeuThrSerAsnGlyThr	516
Qy	1783	---CAAGGGCGTTAGAGATTACATGTAGAACTCCT-----AATTCTACCAATCT	1830
Db	517	LeuSerGlyArgMetGluIleGlnCysLysThrSerIlePheAsnAspProThrArgSer	536
Qy	1831	TATTACATTAGACTTCGATAGCTACAAATGGTGTGGAATATCTCTCTCTTAATATCT	1890
Db	537	TyrGlyLeuArgIleArgTyAlaAlaAsnSerPro-----IleValLeuAsnValSer	554
Qy	1891	CTTACAATACAGGAGTAGTAATAGGAATACCACCTCAACGACTCAACAACTTTTTCGGT	1950
Db	555	TyrValLeuGlnGlyValSerArgGlyThrThrIleSerThrGluSerThrPheSerArg	574
Qy	1951	ACAAATTAAT-----AATAATTAACATACGGAGATTTTGGGTATTTCCAA-----	1998
Db	575	ProAsnAsnIleIleProThrAspLeuLysTyGluGluPheArgTyLysAspProPhe	594
Qy	1999	CCAAGTACGTAACTTACCTTTAAATCGAAAC-----ATACCATTTATATTTAATCGT	2052
Db	595	AspAlaIleValProMetArgLeuSerSerAsnGlnLeuIleThrIleAlaIleGlnPro	614
Qy	2053	GCAGATGTA---TCAAAATTCAAATTTTAAATCATTTGATATAAATTTGATATCAATTA	2109
Db	615	LeuAsnMetThrSerAsnAsnGlnValIleIleAspArgIleGluIleIleProIleThr	634
Qy	2110	TCCTCTGTAGCCCAATAGAGAAAACAAAATATTAGAACTATCCAAACAAAATAAAT	2169
Db	635	GlnSerValLeuAspGluThrGluAsnGlnAsnLeuGluSerGluArgGluValValAsn	654
Qy	2170	ACATTTTTCAAATCATACAAAATACTTTAAATATAGAGCCACAACTATGATATT	2229
Db	655	AlaLeuPheThrAsnAspAlaLysAspAlaLeuAsnIleGlyThrThrAspTyAspIle	674
Qy	2230	GAT 2232	
Db	675	Asp 675	
RESULT 10			
Q8VNX1_BACTV PRELIMINARY; PRT; 688 AA.			
ID	Q8VNX1_BACTV	01-MAR-2002 (TrEMBLrel. 20, Created)	
AC	Q8VNX1	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)	
DT	01-MAR-2002	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	Cry30Aa protein.		
GN	Name=Cry30Aa;		
OS	Bacillus thuringiensis (subsp. medellin).		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;		
OC	Bacillus cereus group.		
OX	NCBI_TaxID=79672;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RL	Delecluse A., Ordaz S.; Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ251978; CAC80986.1; -; Genomic DNA.		
DR	GO; GO:0016787; F:hydrolyase activity; IEA.		
DR	GO; GO:0005102; F:receptor binding; IEA.		
DR	GO; GO:0006952; P:defense response; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	GO; GO:0030435; P:sporulation; IEA.		
DR	InterPro; IPR001178; Endotoxin_C.		
DR	InterPro; IPR005638; endotoxin_C.		
DR	InterPro; IPR005639; endotoxin_N.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		
SQ	SEQUENCE 688 AA; 77844 MW; 780D57085BD7B3A9 CRC64;		
Alignment Scores:			
Pred. No.:	7.18e-46	Length:	688
Score:	801.50	Matches:	244
Percent Similarity:	46.82%	Conservative:	109
Best Local Similarity:	32.36%	Mismatches:	272
Query Match:	20.35%	Indels:	129
DB:	2	Gaps:	30
US-10-782-570-1 (1-2235) x Q8VNX1_BACTV (1-688)			
Qy	13	AAATTAATGAATATGATATATCGAT---TCAAAGAATTTATCTTCTCTAAACAGA	69
Db	6	AsnLysAsnGluTyGluIleLeuAspThrSerGlnLysAsnSerAsnMetSerAsnArg	25
Qy	70	AAATATTGATCATTTAGATACCCCTTACACAAATAATCAAAATCAACCATTAACAAACACA	129
Db	26	-----TyrSerLysTyProLeuThrAsnAsnProLysValProLeuGlnAsnThr	42
Qy	130	AAATTAAGAGCGCTCAATATGTGTCAAGGGGATACACATATGTGTATATTCGAG	189
Db	43	AsnTyLysAspTrpLeuAsnMetCysGlnThrIleThrProLeuCysThrProIleAsp	62

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative mosquitoicidal toxin.
 GN Name=cry30Aa like;
 OS *Bacillus thuringiensis* (subsp. entomocidus).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 CC *Bacillus cereus* group.
 OX NCBI_TaxID=1436;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=INA288;
 RA Ikeya T., Yamaya K., Ito T., Sahara K., Bando H., Asano S.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB125059; BAD00052.1; -; Genomic DNA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0005102; F:receptor binding; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR GO; GO:0030435; P:sporulation; IEA.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF03944; Endotoxin_C; 1.
 DR Pfam; PF00555; Endotoxin_M; 1.
 DR Pfam; PF03945; Endotoxin_N; 1.
 SQ SEQUENCE 683 AA; 77438 MW; 486B477B876BFDCA CRC64;

Alignment Scores:

Pred. No.: 1.69e-45 Length: 683
 Score: 796.00 Matches: 245
 Percent Similarity: 45.13% Conservative: 107
 Best Local Similarity: 31.41% Mismatches: 264
 Query Match: 20.21% Indels: 164
 DB: 2 Gaps: 32

US-10-782-570-1 (1-2235) x Q75VA2_BACTE (1-683)

QY 22 GAATATGAGATTATCGATTCAAGAAATTATCTTCTCTCAACAGAAATATTGATCAT 81
 DB 9 GluYrGluIleuAspAla-----LeuProAsnTyrSerAsnMetValAsnAlaTyr 26
 QY 82 TCTAGATACCCCTTACACAATAATCCAAATCAACATTACAAAACACAAAATTACAAAGAG 141
 DB 27 SerArgTyrProLeuAlaAsnAsnProGlnValProLeuGlnAsnThrSerTyrIysAsp 46
 QY 142 TGGCTCAATATGTGTCAAGGAATACACAATATGTTGATGATAATTCGAGACATTTGCTAGT 201
 DB 47 TrpLeuAsnMetCysGln-----ThrIleAsnPro 56
 QY 202 GCTGATACA-----ATTGCTGCAGTTAGTCAGGTACTATTGTATCCGGT 246
 DB 57 LeuCysThrProIleAsnIleAspIleAspSerIleuAlaSerIleAlaValGly 76
 QY 247 ACTCTGTTAGCGGTATAGTGGGCTCACTTCTATATCCGACCGATAGGAATAATAGGT 306
 DB 77 SerIleLeuAla-----LeuIleProGlyProGlyGluAlaIleGly 90
 QY 307 GCTATAATAATATCTTTGGTACCTTAATCACTGCTTTTGGCCCGCGGAGAACAGAC 366
 DB 91 PheValLeuGlyThrPheSerThrIleLeuProIleLeuTyrProAsnGlyGlu----- 108
 QY 367 AAAACAGTATGACACAATTTATTAAATGGGA--GAATTTTGTGTGATACACCGTTA 423
 DB 109 ThrIysIleThrPheAspPheAlaGluArgGlyLeuGlnLeuPheArgProGluLeuGly 128
 QY 424 ACAGAAAGCATAAACAGCTAAAGTTACAAACTTTAGAAGGATTTAGACAATA----- 477
 DB 129 GlnAspAlaIleGluIleuValThrGlyValIysSerGlyTyrAsnAlaLeuIysAsn 148
 QY 478 ---TTACAAAGCTAATACAGCATAGATGATTGAGAAAATTTAAAGACTACAGCT 534
 DB 149 ArgMetGluAsnPheGluGlnAlaPheThrIysTrpIys----- 161
 QY 535 CTGGATTACCAACCATCATCATCAACAGCTGCCTTGACTCTCTTAAATACGA--- 591

DB 162 ---GlyAsnArgThrArgSerAsnAlaGluGlnVal-----IleArgAsp 175
 QY 592 TTTGAGAATGTTCACATGATTTTATTTCGAGAAATACCTCGTTTCCAACTTGAA---ACT 648
 DB 176 PheAspSerValArgAspIysValIleAspLeuIysAsnAspTyrMetIleAsnProGlu 195
 QY 649 TATAAACGGCTATTACTACCTATTATTATCGGCAAGCTGCTAATTTTTCATTTAAATTTATTA 708
 DB 196 AsnIysProAlaPheIleAsnLeuTyrAlaGlnThrAlaAsnIleAspLeuIleuTyr 215
 QY 709 CAACACAGCTGCTGAATGGCTGATGAATGCAGATATACATCTTCAACAATTCGAA 768
 DB 216 GlnArgGlyAlaValTyrGlyAspAspIleAspIleAsnGlySer---IleSer 234
 QY 769 CCTAATGCTGGAAACATCAGATGACTATTATAAACTTTTAAAGAAAATATATACCTAAATAT 828
 DB 235 ProPheTrpGly---SerIysAspTyrTyrGluSerLeuIysThrIysIleGluGluTyr 253
 QY 829 AGTAACTATTGTGCAATATCTATAGAGAAGGACTAATAAATCTTCGAAACGAACTAAT 888
 DB 254 ThrAsnTyrCysAlaGluThrTyrArgAsnSerLeuAsnIleLeuIysAsnLysProAsn 273
 QY 889 ATGAGATGGAGTATATTAAATGATTATCGAAGATATATGACTATTACTGTATTAGATACT 948
 DB 274 IleSerTrpAspThrTyrAsnLysTyrArgArgGluAlaThrLeuGlyAlaLeuAspLeu 293
 QY 949 ATCGCTCAATTTCTTTTATGATATAAGAGATACAAAGATTCATAGGAGAATAGGT 1008
 DB 294 ValAlaLeuPheProAsnTyrAspMetHisLeuTyrPro-----Ala 307
 QY 1009 GGCATTTAAACTGAACTTACAGAGAAATTTATACAACCTGAATAAATTTTGACCGCTT 1068
 DB 308 AlaThrIysThrGluLeuThrArgLysIleTyrMetProSerPheGlyLeuGlnGlnSer 327
 QY 1069 ACTTACCTTCAATTCACCAATCTCGCTATATGAATATAATTAATAACACGTTCCAGG 1128
 DB 328 AsnTyrPheGln-----SerLeuGluGlyLeuGluAsnAlaLeuThrHisProPro 344
 QY 1129 CTTAGATATTATTTTAGATGAACCTTATATTTTATACAAAATAATGAACGCTACGGG 1188
 DB 345 ---SerLeuPheThrTyrLeuAsnGluLeuAsnLeuTyrThrValArgGluAsnPheAsn 363
 QY 1189 -----AATCGTTTGTGTTGTTGCGAATCGTAAATAGATCTACTATTGCT 1233
 DB 364 ProAlaLeuGlnValSerSerLeuSerGlyLeuGlnAlaArgSerArgTyrThrGlnAsn 383
 QY 1234 ACACAGGAACCTGAA---ATTATATATGGAGAAAGACAGCTCCACCAACAAAAA 1290
 DB 384 ProThrIleLeuAspAsnProAlaGlnGlyValArgAsnGlyThrSerThrGlnIleGly 403
 QY 1291 TTAATACCATTTGAATCTATAAAGTTTCAATTGTAACTCATAGACAAAGTAACCTCTACT 1350
 DB 404 LeuAsnAsnLeuPheValTyrIysLeuSerMetSerGlnTyrHisHisProAsnAspCys 423
 QY 1351 TCCCTTTTCTCAACATATCTTTACAAATTAACTCAATTCAAATTGAACTTTAT-----TTA 1401
 DB 424 SerSerIleAlaGly-----IleSerAspMetThrPheTyrIysSerAspTyr 439
 QY 1402 AATAATTCACCTAGTATAATAATAACATATTTCAGCTGGGGGAATTTATCTAATGATAAA 1461
 DB 440 AsnGlyAsnAlaSerAlaThrGlnThrTyrGlnAlaGlyArgAsnThrAsnAsn----- 457
 QY 1462 AAAACAACTGATTTTCAATTTCTGTAAAAAAGACGTGTAACCAATTTATTAAT----- 1515
 DB 458 -----ValIleAsnThrPhe 462
 QY 1516 -----CCAAATTTTACCAGCTATAATAGTTATAGT-----CAT 1551
 DB 463 MetAsnGlyProGlnIysAlaSerSerSerAsnAsnIleSerIleIysGlnThrLysHis 482
 QY 1552 ATTTTATCCCAAGTTTCTTTA----- 1572

Db 483 lleLeuSerAspIleLysMetIleTyrPheArgThrGlyGlyMetTyrGlnValTyrAsp 502
 QY 1573 TTTAATTATCTTAAATTTGGATTAGCGCTAAATATATATATATATACAGTGCATTAGGA 1632
 Db 503 PheGlyTyrSerPhe-----Ala 508
 QY 1633 TGGACACACAGTAGTGTAAATAGAAATTAATGCAATATCAGATATAAATAATACAAATGATC 1692
 Db 509 TrpThrHisThrSerValAspProAspSerValValValValValValValValValValVal 528
 QY 1693 CCAGCAATCAAGGTAAACAGCTTTCATCAAACTCAAGTAAAGTAAATGAAGGACCTGGTCAT 1752
 Db 529 ProAlaValLysAlaLeuGlyIleSerThrAspSerLysValValValValValValValValVal 548
 QY 1753 ACAGAGCAAACTGGTTTATTATCAAAAGTCAAGGCGCTTTAGAGATACATGATGAGAACT 1812
 Db 549 lleGlyGlyAspLeuLeuLeuLysLeuGlnAlaThrIleArgIle-----LysThr 566
 QY 1813 CCTAATTCACCAATCTTATACATTAGACTTCGATACGCTACAAATGGTGTGCGAAAT 1872
 Db 567 AspHisAlaAsnThrArgTyrLysIleArgValArgTyrAlaSerAsn-----AlaAsn 584
 QY 1873 ACT-----CTTCCTAAT---ATATCTTACAAATACAGGAGTAATA 1911
 Db 585 ThrProIleValLeuSerSerLeuGlnAsnThrLeuThrValThrPhePro----- 601
 QY 1912 GGNATACCACTCAAGACTCAACAACTTTTCTGCTACAAATTAATAATTTACAA 1971
 Db 602 -i-----GlnThrIleThrHisSerThrIleSerGluLeuGln 613
 QY 1972 TACGAGAGTTTGGTATTTCCAAATTCAGTACAGTAAACATTTTAAATCGAAAC 2031
 Db 614 TyrLysAspPheGlnTyrValThrPheProGly----- 624
 QY 2032 ATACCAATTAATTTAATCGTCAGATGTATCAAAATTCAAAT 2073
 Db 625 ---GluPheIleMetAspLysProSerIleAspValAlaIleArgGlyValGlnAsnAsp 643
 QY 2074 -----TTAATCAATTTGATAAAATTTGATTTTATACCAATTTCTCTGTAGCCAA 2124
 Db 644 ArgAsnAspIleTyrIleAspArgIleGluPheLeuProIleThrGlnSerValLeuAsp 663
 QY 2125 AATAGAGAAACAAAATAAGTAATACTATCAACAAAATAATAATATATTTTCACAAT 2184
 Db 664 TyrThrGluGluGlnAsnIleGluLysSerGlnLysAlaValAsnAspLeuPheIleAsn 683

RESULT 12

CR8BA BACUK STANDARD; PRT; 1169 AA.
 ID CR8BA BACUK STANDARD; PRT; 1169 AA.
 AC Q45705;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Peptide crystal protein cry8Ba (Insecticidal delta-endotoxin
 DE CryIIIB(a)) (Crystalline entomocidal protoxin) (134 kDa crystal
 DE protein)
 GN Name=cry8Ba; Synonyms=50C(b), cryIIIB(a);
 OS Bacillus thuringiensis subsp. kumamotoensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=132267;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=NRRL B-18746 / PS50C;
 RA Michaelis T.E., Poncerra L., Narva K.E.;
 RT "Process for controlling scarab pests with Bacillus thuringiensis
 RT isolates";
 RL Patent number WO9315206, 05-AUG-1993.
 CC -i- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
 CC epithelial cells of insects. Active on various scarabaeid beetles.
 CC -i- DEVELOPMENTAL STAGE: The crystal protein is produced during
 CC sporulation and is accumulated both as an inclusion and as part of
 CC the spore coat.

CC -i- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
 CC -i- SIMILARITY: Belongs to the delta endotoxin family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; U04365; AAA21118.1; -; Genomic_DNA.
 DR HSSP; P07130; 1DLC.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF03944; Endotoxin_C; 1.
 DR Pfam; PF00555; Endotoxin_M; 1.
 DR Pfam; PF03945; Endotoxin_N; 1.
 KW Sporulation; Toxin.
 SQ SEQUENCE 1169 AA; 133544 MW; 22BEFCF5BD699909 CRC64;
 Alignment Scores:
 Pred. No.: 6.82e-45 Length: 1169
 Score: 787.50 Matches: 216
 Percent Similarity: 47.55% Conservative: 152
 Best Local Similarity: 27.91% Mismatches: 297
 Query Match: 19.99% Indels: 109
 DB: 1 Gaps: 28
 US-10-782-570-1 (1-2235) x CR8BA_BACUK (1-1169)
 QY 1 GTGAATCAAAATATAATTAATGAATATGAGTATCGATTCAAGAATTTATCTATCCT 60
 Db 1 MetSerProAsnAsnGlnAsnGluTyrGluIleLeuAspAlaThrProSerThrSerVal 20
 QY 61 TCTAACCAAAATATTGATCATTCTAGATACCTTACACAAATATATCCAAATCAACCATTA 120
 Db 21 SerAsn-----AspSerAsnArgTyrProPheAlaAsnGluProThrAsnAlaLeu 37
 QY 121 CAAACCAAAATTAACAAGAGTGGCTCAATATGTGTCAAGGGAAT---ACACAATATGCT 177
 Db 38 GlnAsnMetAspTyrLysAspTyrLeuLysMetSerAlaGlyAsnValSerGluTyrPro 57
 QY 178 GATAATTCGAGACATTTGCTAGTCTGATACAAATTCGTCAGTGTAGTACAGGTACTATT 237
 Db 58 GlySerProGluValPheLeuSerGluGlnAsp-----AlaValLysAlaAlaLeuAsp 75
 QY 238 GTATCCGGTACTCTGTAGCGGTATAGTGGGCTCACTTCTATATCCGACCGATAGGA 297
 Db 76 lleValGlyLysLeuLeuThrGlyLeuGly-----ValPro 87
 QY 298 ATAATAGTGTCTATAATAATATCTTTGGTACCTTAATCTCTCTTTTGGCCCGCGGA 357
 Db 88 PheValGlyProIleValSerLeuTyrThrGlnLeuIleAspIleLeuTyrProSer--- 106
 QY 358 GAACAGACAAACAGTATGACACAAATTTATTAATGGAGGAATTTTGTTCATACA 417
 Db 107 ---LysGlnLysSerGlnTyrPheMetGluGlnValGluGluLeuIleAsnGln 125
 QY 418 CCGTTTACAGAAAGCATAAACAGCTAAAGTATACAACTTTTAGAAGGATTTAGACAAATA 477
 Db 126 LysIleAlaGluTyrAlaArgAsnLysAlaLeuSerGluLeuGluGlyLeuLysAsnAsn 145
 QY 478 TTACAAAGCTATAATACAGCAATTAGATTTGGAGAAATTTAAAGACTCAAGCTCCT 537
 Db 146 TyrGlnLeuTyrLeuThrAlaLeuGluGluTyrLysGlu----- 158
 QY 538 GGATTACCAACCATCATCAGCAATTCACAAAGCTCCCTTGACTCTTAAATACGATTGAG 597
 Db 159 -----AsnProAsnGlySer-----ArgAlaLeuArgAspValArgAsnArgPheGlu 174
 QY 598 AATGTTTCAATGATTTTATTCGAGAAATACCTCGTTTCCAACTTGTAAACTTATATAACG 657
 Db 598 AATGTTTCAATGATTTTATTCGAGAAATACCTCGTTTCCAACTTGTAAACTTATATAACG 657

Db 175 IleLeuAspSerLeuPheThrGlnTyrMetProSerPheArgValThrAsnPheGluVal 194
QY 658 CTATTACTACCTATTTATGCGCAAGCTGCTAAATTTTCATTTTAAATTTATTAACAAGGT 717
Db 195 ProPheLeuThrValTyrThrMetAlaAsnLeuHisLeuLeuLeuLeuLeuArgAspAla 214
QY 718 GCTGAATGGCTGATGAATGAATGCAGATATACATCTCTCACAAATGAACCTAAATGCT 777
Db 215 SerIlePheGlyGluThrGlyLeu-----SerThr 225
QY 778 GGAACATCAGATGACTATTATAAACTTTTAAAGAAATATATACCTAAATATAGTAACCTAT 837
Db 226 SerThrIleAsnAsnTyrTyrAsnArgGlnMetLysLeuThrAlaGluTyrSerAspHis 245
QY 838 TGTGCAAACTACTAGAGAGGACTAAATAACTTCGAAACGAACCTAAATATAGATGG 897
Db 246 CysValLysTyrTyrGluThrGlyLeuAlaLysLeuLysGlySerSerAlaLysGlnTyr 265
QY 898 AGTATATTAATGATTATCGAAGATATATGACTATCTGATCTATAGTATAGTACTATCGTCAA 957
Db 266 IleAspTyrAsnGlnPheArgGluMetThrLeuThrValLeuAspValAlaLeu 285
QY 958 TTTTCTTTTATGATATAGAGATACAAAGATTCAATAGCAAGTAAAGTGGCATAAA 1017
Db 286 PheSerAsnTyrAspThrArgThrTyrProLeuAla-----ThrThr 299
QY 1018 ACTGAACCTACAGAGAAATTTATACACTGAAATAAATTTTGACGGCTTTACTTACCTT 1077
Db 300 AlaGlnLeuThrArgGluValTyrThr-----AspProLeuGlyAlaVal 314
QY 1078 GAAATTCACCAACTCTC-----GCTATAATGGAATATAATTTAAACA 1119
Db 315 AspVal-----ProAsnIleGlySerTyrTyrAspLysAlaProSerPheSerGluIleGlu 333
QY 1120 CGTTCAGGCTTAGA-----TTATTTTCATTTTATAGTGAACCTATATTTTATACA 1170
Db 334 LysAlaAlaIleArgProHisValPheAspTyrIleThrGlyLeuThrValTyrThr 353
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Db 354 LysLysArgSerPheThrSerAspArgTyrMetArgTyrTrpAlaGlyHisGlnIleSer 373
QY 1228 TATGCTACGACAGCAAGCAATATATATATGAGAGAACAGCTCCACCCACACAAAA 1287
Db 374 TyrLysHisIleGlyThrSerSerThrPheThrGlnMetTyrGly-----ThrAsnGln 391
QY 1288 ACTTTA-----ATACCATTTGAATCTCTATAAAGTT---TCAATTTGTAAT 1329
Db 392 AsnLeuGlnSerThrSerAsnPheAspPheThrAsnTyrAspIleTyrLysThrLeuSer 411
QY 1330 GATAGACAAGTAATCTCTACTTCCCTCTTCTTCTAACATA----- 1368
Db 412 AsnGlyAlaValLeuLeuAspIleValTyrProGlyTyrThrTyrThrPhePheGlyMet 431
QY 1369 -----TACTTTTACAATTAATCAATTAATGAACCTTTATTTAAATTAATTCACCTAGT 1416
Db 432 ProGluThrGluPhePheMetValAsnGlnLeu-----AsnAsnThrArg 446
QY 1417 AATAAATTAACATATTCA---GCTGGGGGGAATTTATCTATGATATAAAAAACAATCAT 1473
Db 447 LysThrLeuThrTyrLysProAlaSerLysAspIleIleAspArgThrArgAspSerGlu 466
QY 1474 TTTCAATTTCTGTAAAAAAAGACTGTAAACAATATTATATCCAAATGTTTATCCAGC 1533
Db 467 LeuGluLeuProGluThrSerGlyGln-----ProAsn 478
QY 1534 TATAATAGCTTAGTCATATTTATCCAGCTTTCTTTTATTTATTAATTTCTCTATAAAT 1593
Db 479 TyrGluSerTyrSerHisArgLeuGlyHisIleThr-----PheIleTyrSer----- 494
QY 1594 GGATTAGCGCTAAATATATATATATACAGGTCGATTTAGGATGGACACACAGTAGTGTAA 1653
Db 495 -----SerSerThrSerThrTyrValProValPheSerTyrTrpHisArgSerAlaAsp 512

QY 1654 AGAATAATCAATATCAGATATAAAATAATTAATCAATGATCCAGCAATCAAGGTAACAGT 1713
Db 513 LeuThrAsnThrValLysSerGlyGluIleThrGlnIleProGlyGlyLysSerSerThr 532
QY 1714 CTTGATACAACTCTAAGGTAATTTGAAGGACCTGGTCATACAGGAGGAAACTTGGTTTAT 1773
Db 533 IleGlyArgAsnThrTyrIleIleLysGlyArgGlyTyrThrGlyGlyAspLeuValAla 552
QY 1774 TTCAAAAGTCAA---GGCGCTTTAGAGATTACATGTAGAACTCTCTAAATTTCTACAATCT 1830
Db 553 LeuThrAspArgIleGlySerCysGluPheGlnMetIlePheProGluSer---GlnArg 571
QY 1831 TATTACATTAGACTTCGATACGCTCAAAATGGTGGTCTGGAATATCTCTCTCTAATATATCT 1890
Db 572 PheArgIleArgIleArgTyrAlaSerAsnGluThrSer-----Tyr 585
QY 1891 CTTACAATACAGGAGTAATAGGAATACCACCTCAACGACTCAACACACATTTTCTCTGGT 1950
Db 586 IleSerLeuTyrGlyLeuAsnGlnSerGlyThrLeuLysPheAsnGlnThrTyrSerAsn 605
QY 1951 ACAATATTATTAATTTACAATACGAGATTTTGGGTATTTTCCAATTTCCAAGTACAGTA 2010
Db 606 LysAsnGluAsnAspLeuThrTyrAsnAspPheLysTyrIleGluTyrProArgValIle 625
QY 2011 ACATTACTTTAAATCGAAACATACCATTTATATTTAATCGTCGAGATGTATCAATTC 2070
Db 626 SerValAsnAlaSerSerAsnIleGlnArgLeuSerIleGlyIleGlnThrAsnThrAsn 645
QY 2071 ATTTTAATCATTTGATAAAATTTGAATTTATACCAATTAATCTCTCTGTACGCAAAATAGA 2130
Db 646 LeuPheIleLeuAspArgIleGluPheIleProValAspGluThrTyrGluAlaGluThr 665
QY 2131 GAAAAACAAAATTTAGAACTATCCAAACAAAATAAATACATTTTTCACAAATCATACA 2190
Db 666 Asp-----LeuGluAlaAlaLysLysAlaValAsnAlaLeuPheThrAsn---Thr 681
QY 2191 AAAAATACTTTAAATATATAGAACCCCAACATCATGATTTGAT 2232
Db 682 LysAspGlyLeuGlnProGlyValThrAspTyrGluValAsn 695
RESULT 13
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ID Q5W7N9_BACTU PRELIMINARY; PRT; 688 AA.
AC Q5W7N9;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DS Cry30-like.
OS Bacillus thuringiensis.
OC Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC SPRAIN-96-OK-85-24;
RA Oigushi A., Wasano N., Saitoh H., Ohba M.;
RT "Identification and characterization of novel cry genes from an
RT mosquito-specific Bacillus thuringiensis serovar sotto strain."
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB193814; BAD67157.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 688 AA; 77438 MW; D5F1C265AEC6CBD1 CRC64;

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943	GAT	ACT	AT	C	G	C	T	C	CA	A	T	T	T	T	T	T	T	T	T	T	1002
292	Asp	Leu	Ala	Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Ile	Cys	Ile	Tyr	Pro	Ile	Gln	-----	----	308	
1003	AT	AG	T	G	G	C	A	T	T	A	A	A	C	T	T	A	C	A	G	A	1062
309	-----	Th	r	L	y	S	h	r	G	l	u	e	u	r	A	r	g	L	e	u	325
1063	CG	T	C	T	A	C	T	T	G	A	A	T	T	C	A	A	C	C	A	A	1122
326	Gln	Ser	Asn	Tyr	Phe	Gln	-----	Ser	Leu	Glu	Gly	Leu	Ala	Leu	Ala	Leu	Thr	His	342		
1123	TC	AG	G	G	C	T	A	G	A	T	T	T	C	A	T	T	T	T	T	A	1182
343	Pro	Pro	-----	Ser	Leu	Phe	Thr	Trp	Leu	Asn	Glu	Leu	Asn	Leu	Tyr	Thr	Ile	Arg	Glu	361	
1183	TAC	GGG	-----	A	N	C	G	T	T	A	G	T	T	G	G	T	A	T	-----	1206	
362	Phe	Asn	Pro	Ala	Leu	Leu	Val	Ser	Ser	Leu	Ser	Gly	Leu	Gln	Ala	Ile	Ser	Arg	Tyr	381	
1207	GCG	AA	T	C	G	T	A	T	A	G	A	T	C	T	T	A	T	T	A	T	1266
382	Gln	Asn	Pro	Asn	Arg	Ile	Ser	Asn	Pro	Ala	Gln	Gly	Val	-----	Arg	395					
1367	AC	AG	T	C	C	A	C	C	A	C	A	A	A	A	C	T	T	A	A	T	1326
396	Asn	Gly	Thr	Pro	Thr	Gln	Ile	Gly	Leu	Asn	Asn	Leu	Phe	Val	Tyr	Leu	Ser	Leu	-----	414	
1327	ACT	G	A	T	A	G	A	C	A	G	P	A	C	T	C	T	T	C	C	C	1380
415	-----	Ser	Gln	Tyr	His	His	Pro	Asn	Glu	Cys	Tyr	Ser	Ile	426							
1381	AAT	CAA	ATT	-----	G	A	C	T	T	A	T	T	A	A	T	A	T	T	C	C	1419
427	Ala	Gly	Ile	Ser	Asp	Met	Thr	Phe	Tyr	Lys	Ser	Asp	Tyr	Asn	Gly	Asn	Ala	Pro	Thr	446	
1420	AA	A	T	T	A	C	A	T	A	T	C	A	G	T	G	G	G	A	A	T	1479
447	Gln	-----	Thr	Tyr	Gln	Ala	Gly	Arg	Asn	-----	Ser	Asn	Asn	Phe	Ile	Asn	Thr	Phe	Met	464	
1480	T	T	C	T	C	T	G	T	A	A	A	A	A	G	A	C	T	G	T	A	1539
465	Gly	Pro	Gln	Glu	Ala	Ser	Ser	Ser	Asn	Asn	Ile	-----	Ser	Ile	Lys	478					
1540	A	G	T	A	T	A	G	T	A	T	T	T	T	A	T	T	T	T	T	A	1599
479	Gln	Thr	Asn	His	Ile	Leu	Ser	Asp	Ile	Lys	Met	Ile	-----	Tyr	Ser	Arg	Thr	Gly	Ile	497	
1600	G	C	G	C	T	A	A	T	A	T	A	T	A	C	A	G	T	G	C	A	1659
498	Tyr	Pro	Ser	Tyr	Asp	Phe	Gly	Tyr	Ser	Phe	Ala	Trp	Thr	His	Thr	Ser	Val	Asn	Pro	517	
1660	A	A	T	C	A	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	1719
518	Asn	Leu	Ile	Val	Pro	Asn	Arg	Ile	Thr	Gln	Ile	Pro	Ala	Val	Val	Ala	Asp	Tyr	Leu	537	
1720	A	C	A	A	C	T	A	A	G	T	A	A	T	T	A	A	G	A	C	T	1776
538	Ser	Pro	Ala	Lys	Val	Ile	Ala	Gly	Pro	Gly	His	Thr	Gly	Asp	Leu	Val	Ala	Leu	Leu	557	
1777	-----	C	A	A	G	T															

Db 294 LysAlaGluLeuThrArgGluIleTyrSerAspValIleAsn---AspHisValTyrGly 312
QY 1075 CTTGAAATTCACCAATCTCGCTATA-----ATGGATATATAATTTAAACAGTTTCAGGG 1128
Db 313 LeuMetVal---ProTyrIleSerPheGluHisAlaGluSerLeuTyrThrArgArgPro 331
QY 1129 CTTAGATTATTTTCATTTTATAGTAACTTATATATTTATACAAAATTTGAAACGTACGGG 1188
Db 332 ---HisAlaPheThrTrpLeuIleGlyPheArgPheValThrAsnSerIleAsnSerTrp 350
QY 1189 AATCGTTAGTTGGTATTCGAAATCGTAATAGATCTACTTATGTCACGACAGGAAGTAA 1248
Db 351 ThrPheLeuSerGlyGlyGluAsnArg-----TyrPheLeuThrHisGlyGlyGluGly 367
QY 1249 ATTATATAT-----GGAGAAAGAACAGGTCCACCCACACAAACAACTTTA 1293
Db 368 ThrIleTyrAsnGlyProPheLeuGlyGlnAspThrGluTyrGlyThrSerSerTyr 387
QY 1294 ATACCATTTGAATCC-----TATAAAGTTTCAATTTGTAACCTGATAGACAAGTA 1341
Db 388 IleAspIleSerAsnAsnSerSerIleTyrAsnLeuTrpThrLysAsnTyrGluTrpIle 407
QY 1342 ACTCCT---ACTCCCTC-----TTTCCTAACATATATCTTACAAATTAATCAAAATTGAA 1392
Db 408 TyrProTrpThrAspProValAsnIleThrLysIleAsnPheSerIleThr----- 424
QY 1393 CTTTATTAAATATTCACCTAGTAAATTAATTAATATTCATATTCAGCTGGGGGAAATTATCT 1452
Db 425 ---AspAsnSerAsnSerSerGluSerIleTyrGlyAla---GluArgMetAsn 440
QY 1453 AATGATAAAAAACAACTGATTTTCAATTTCTCTGTAAAAAAGACTGTAAACCAATTATT 1512
Db 441 LysProThrValArgThrAspPheAsnPheLeuLeuAsnArg----- 454
QY 1513 AATCAAAATTTGTTTCAAGCTATATATAGTTATAGTATATTTATCCAGTTTCTTTA 1572
Db 455 AlaGlyAsnGlyProThrThrTyrAsnAspTyrAsnHisIleLeuSer---TyrMetLeu 473
QY 1573 TTTAAT-----TATTCCTATAAATTTGGATTAGCG 1602
Db 474 IleAsnGlyGluThrPheGlyGlnLysArgHisGlyTyrSerPhe----- 488
QY 1603 CTAAATATATATATATACAGGTGCTATAGGATGGACACACAGTAGTGTAAATAGAAATAAT 1662
Db 489 -----AlaPheThrHisSerSerValAspArgTyrAsn 499
QY 1663 GCAATATCAGATAAAATAATTAACAATGATCCAGCAATCAAGGTAACAGTCTTGATACA 1722
Db 500 ThrIleValProAspLysIleValGlnIleProAlaValLysThrAsnLeuValGlyAla 519
QY 1723 AACTCTAAGTAAATGAAGACCTGGTCTATACAGGAGGAACCTGGTTTATTTTACAAAGT 1782
Db 520 Asn-----IleIleLysGlyProGlyHisThrGlyGlyAspLeuLysLeuGluTyr 537
QY 1783 CAAGGGCGTTTATAGATTACATGTAGAACTCTTAATTTCTACACAATCTTATTACATAGA 1842
Db 538 GluArgPheLeuSerLeuArgIleLysLeu---IleAlaSerMetThrPheArgIleArg 556
QY 1843 CTTTCATAGCTACAAATGGTCTGGAAATATCTTCTCTTAATATATATCTCTTACAAATCCA 1902
Db 557 IleArgTyrAlaSerAsnIleSerGlyGlnMetMetIleAsnIleGlyTyrGlnAsnPro 576
QY 1903 GGAGTAATAGGAATACCACTCAACGACTCAACACACTTTTCTGGTGAATATATAT 1962
Db 577 ThrTyrPheAsnIleIleProThr-----ThrSerArgAspTyrThr 590
QY 1963 AATTTCATATACCGAGATTTGGG-----TATTTCCAAATTTCCA 2001
Db 591 GluLeuLysPheGluAspPheGlnLeuValAspThrSerTyrIleTyrSerGlyGlyPro 610
QY 2002 AGTACAGTAACATTACCTTTAAATCCGAAACATACCACTTATATTTAATCGTCGAGATGTA 2061
Db 611 Ser-----IleSerSerAsnThrLeuTrpLeuAspAsn-----Phe 622

QY 2062 TCRAATTCAAATTTTAATCAATGATAAAATTCGAATTTATACCAATTCCTCTCTGTACGC 2121
Db 623 SerAsnGlyProValIleIleAspLysIleGluPheIleProLeuGlyIleThrLeuAsn 642
QY 2122 CAAATAGAGAAAACAAAATTAAGAACTATCCAAACAAAATAAATATACATTTTTCACA 2181
Db 643 Gln-----AlaGlnGlyTyrAspThrTyrAspGlnAsnAlaAsnGlyMetTyrHis 659
QY 2182 AATCATCAAAAATATCT-----TTAAATATAGAAGCCACAAACTAT 2223
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RESULT 15
ID Q56B08_BACTU PRELIMINARY; PRT; 1169 AA.
AC Q56B08;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Crystal protein Cry9Db1.
GN Name=cry9Db1;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC FLANNAGAN-DP1019;
RA Flannagan R.D., Abad A.R.;
RT "Bacillus Cry9 Family Members."
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY971349; AAX78439.1; -; Genomic DNA.
SQ SEQUENCE 1169 AA; 132126 MW; 85DC06D5083E3F43 CRC64;
Alignment Scores:
Pred. No.: 1.55e-39 Length: 1169
Score: 708.50 Matches: 225
Percent Similarity: 43.25% Conservative: 134
Best Local Similarity: 27.11% Mismatches: 262
Query Match: 17.99% Indels: 209
DB: 2 Gaps: 34
US-10-782-570-1 (1-2235) x Q56B08_BACTU (1-1169)
QY 1 GTGAATCAAAATAATAATAATGAATATGAGATTATCGATTCAAGAAATTTATCTATCT 60
Db 1 MetAsnArgAsnHisGlnAsnGluTyrGluIleIleAspAlaProHisCysGlyCysPro 20
QY 61 TCTAACAGAAATATTGATCATCTTAGATACCTCTTACACAAATAATCCAAATCAACATT 120
Db 21 SerAsp-----AspValValLysTyrProLeuThrAspAspProAsnAlaGlyLeu 37
QY 121 CAAAACACAAATTAACAAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGTTGAT 180
Db 38 GlnAsnMetAsnTyrLysGluTyrLeuGlnMet-----TyrGlyGly 51
QY 181 AATTTTCGAGACATTTGCTAGTCTGCTATACAATTTGCTGAGTTAGTCAGGTACTATTGTA 240
Db 52 AspTyr-----ThrAspProLeuIleAsnProAsnLeuSerVal 64
QY 241 TCCGGTACTCTGTTAGCCGGTATAGTGGCTCACTTCTATATCCGACCGGATAGGAATA 300
Db 65 SerGlyLysAspValIleGlnValGly-----IleAsnIle 76
QY 301 ATAGTGTCTATAATATATCTTTTGGT----- 327
Db 77 ValGlyArgLeuLeuSerPhePheGlyPheProPheSerSerGlnTrpValThrValTyr 96
QY 328 ---ACCTAATCACTGTCTTTTGGCCCGGGAGAACAGACAAACAGTATGGACACAA 384
Db 97 ThrTyrLeuLeuAsnSerLeuTrpPro-----AspAspGluAsnSerValTrpAspAla 114

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 12, 2006, 06:12:53 ; Search time 184.5 Seconds
(without alignment)

10645.112 Million cell updates/sec

Title: US-10-782-570-1

Perfect score: 3939

Sequence: 1 gtgaatcaataataataa.....caaatgatattgattaa 2235

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+_n2p.model -DEV=xlp
-Q=/cgm2_1/USPTO_epool_p/US10782570/runat_12012006_060221_7509/app_query.fasta_1.2375
-DB=A Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10782570 -CGN_1_260 @runat_12012006_060221_7509 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=120 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A Geneseq_21.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3902	99.1	744	ADR89397	Adr89397 AXMI-007.
2	3623	92.0	694	ADR89399	Adr89399 AXMI-007
3	3314	84.1	735	ADR89395	Adr89395 AXMI-006.
4	1159	29.4	1180	AAp93715	AAp93715 Delta-end
5	1158	29.4	1180	ADR89426	Adr89426 cry4aa.1
6	1157	29.4	1016	AAp94035	AAp94035 Delta-end
7	1157	29.4	1180	AAp82589	AAp82589 Insectici
8	1153	29.3	1180	AAr14373	AAr14373 Dipteran
9	1153	29.3	1180	AAr63078	AAr63078 B.t. toxi

10	901	22.9	1109	5	AAE26353	Aae26353 Bacillus
11	901	22.9	1109	7	ADF31302	Adf31302 Bacillus
12	901	22.9	1109	7	ADF31307	Adf31307 Bacillus
13	900	22.8	686	2	AAR63079	Aar63079 B.t. toxi
14	899	22.8	675	2	AAR14374	Aar14374 Dipteran
15	897	22.8	675	8	ADR89431	Adr89431 cry10Aa.
16	897	22.8	675	9	ADY59866	Ady59866 Bacillus
17	819	20.8	1136	5	AAU76029	Aau76029 Bacillus
18	819	20.8	1136	8	ADR89427	Adr89427 cry4Ba.1
19	819	20.8	1136	9	AEA61391	Aea61391 Bacillus
20	818	20.8	1136	1	AAp93341	AAp93341 Sequence
21	816	20.7	1136	1	AAp82314	AAp82314 Bacillus
22	787.5	20.0	1169	2	AAW06417	AAW06417 Antiscara
23	772.5	19.6	1095	1	AAp97052	AAp97052 Sequence
24	755	19.2	1178	1	AAp60051	AAp60051 Bacillus
25	716	18.2	1210	5	AAU99256	Aau99256 Bacillus
26	716	18.2	1210	8	ADL15307	Adl15307 B thuring
27	716	18.2	1210	9	AEb45609	Aeb45609 B. thurin
28	709	18.0	682	8	ADR89433	Adr89433 cry19Ba.
29	708.5	18.0	780	9	AEA81472	Aea81472 Bacillus
30	708.5	18.0	1169	9	AEA81468	Aea81468 Bacillus
31	706	17.9	651	2	AAW06460	AAW06460 BtPGS1208
32	706	17.9	651	2	AAW06419	AAW06419 Antiscara
33	706	17.9	659	2	AAy23213	AAy23213 Amino aci
34	706	17.9	659	8	ADR89424	Adr89424 cry3Ba.1
35	700	17.8	652	3	AAy23211	AAy23211 Amino aci
36	700	17.8	652	3	AAy70442	AAy70442 Bacillus
37	700	17.8	652	6	ABU09193	ABU09193 Bacillus
38	700	17.8	652	7	ABW01051	ABW01051 Bacillus
39	699	17.7	1206	5	AAU99255	Aau99255 Bacillus
40	699	17.7	1206	8	ADL15305	Adl15305 B thuring
41	699	17.7	1206	9	AEb45607	Aeb45607 B. thurin
42	695	17.6	651	2	AAr33769	Aar33769 Bt isolat
43	693	17.6	652	3	AAy70443	AAy70443 Synthetic
44	693	17.6	652	3	ABU09194	ABU09194 Bacillus
45	693	17.6	652	7	ABW01052	ABW01052 Bacillus

ALIGNMENTS

RESULT 1

ADR89397

ID ADR89397 standard; protein; 744 AA.

XX ADR89397;

XX AC

DT 18-NOV-2004 (first entry)

XX DE

XX AXMI-007.

KW delta-endotoxin; delta-endotoxin associate polypeptide;

KW expression cassette; transformation; transgenic; plant; bacteria;

KW lepidoptera; coleoptera; pest; pesticide; resistance;

KW pesticidal activity.

XX OS Bacillus thuringiensis.

XX XX

FX Key Location/Qualifiers

FT Misc-difference 1

FT /note= "encoded by GTG"

XX XX

XX WO2004074462-A2.

XX PD 02-SEP-2004.

XX XX

XX 20-FEB-2004; 2004WO-US005829.

XX PR

XX 20-FEB-2003; 2003US-0448632P.

XX PR

XX 20-FEB-2003; 2003US-0448633P.

XX PR

XX 20-FEB-2003; 2003US-0448797P.

XX PR

XX 20-FEB-2003; 2003US-0448806P.

XX PR

XX 20-FEB-2003; 2003US-0448810P.

XX PR

XX 20-FEB-2003; 2003US-0448812P.

PR 19-FEB-2004; 2004US-00781979.
 PR 19-FEB-2004; 2004US-00782020.
 PR 19-FEB-2004; 2004US-00782096.
 PR 19-FEB-2004; 2004US-00782141.
 PR 19-FEB-2004; 2004US-00782570.
 PR 19-FEB-2004; 2004US-00783417.
 XX (ATHE-) ATHENIX CORP.
 PA
 XX Carozzi N, Harglass T, Koziel MG, Duck NB, Carr B;
 PI N-PSDB; ADR89396.
 XX WPI; 2004-635574/61.
 DR N-PSDB; ADR89396.
 XX
 PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
 PT for producing organisms with pesticide resistance.
 XX
 PS Claim 12; SEQ ID NO 9; 178pp; English.
 XX
 CC This sequence represents an isolated delta-endotoxin. Some of the delta-
 CC endotoxin coding sequences of the invention have alternative start
 CC codons, producing more than one protein from a single open reading frame.
 CC The nucleic acid sequences of the invention are useful in DNA constructs
 CC or expression cassettes for transformation and expression in plants and
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for
 CC killing lepidopteran or coleopteran pests. Compositions containing the
 CC delta-endotoxins of the invention, and methods for their production, are
 CC useful for the production of organisms with pesticide resistance,
 CC specifically bacteria and plants. These organisms are useful for
 CC generating altered or improved delta-endotoxin or delta-endotoxin-
 CC associated proteins that have pesticidal activity, or for detecting the
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
 CC nucleic acids in products or organisms.
 XX
 SQ Sequence 744 AA;
 Alignment Scores:
 Pred. No.: 0 Length: 744
 Score: 3902.00 Matches: 743
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.87% Mismatches: 0
 Query Match: 99.06% Indels: 0
 DB: 8 Gaps: 0
 US-10-782-570-1 (1-2235) x ADR89397 (1-744)
 QY 1 GTGAATCAAAATAAATAATGAATATGAGATTATCGATTCAAGAATTTATCTATCCT 60
 DB 1 MetAenGlnAenAenAenAenGluTyGluileileaspSerlyAenLeuSerTyPro 20
 QY 61 TCTAACAGAAATATTGATCATCTTAGATACACCTTACACAAATAATCCAAATCAACATTA 120
 DB 21 SerAenArgAenileAenHisSerArgTyProTyThrAenAenProAenGlnProLeu 40
 QY 121 CAAACACAAATTAACAGAGTGGCTCAATGTGTCAAGGGAATACACATATGGTGAT 180
 DB 41 GlnAenThrAenTyLysGluTrpLeuAenMetCysGlnGlnTyAenThrGlnTyGlyAasp 60
 QY 181 AATTTCGAGACATTTGCTAGTGTGATACAAATTCGTCAGTGTAGTCAGGTPACTATTGTA 240
 DB 61 AenPheGluThrPheAlaSerAlaAenThrilealaalavalSerAlaGlyThrileVal 80
 QY 241 TCCGGTACTCTGTAGCCGGTATAGTGGGCTCACTTCTATATCCGGACCGGATAGGAATA 300
 DB 81 SerGlyThrLeuLeuAlaGlyileGlyGlyLeuThrSerileSerGlyProileGlyile 100
 QY 301 ATAGTGTATATAATATCTTTGGTACCTATCACTGTCITTTGGCCCGCGGGAGAA 360
 DB 101 IleGlyAlaileileileSerPheGlyThrLeuileThrValPheTrpProAlaGlyGlu 120
 QY 361 CAAGACAAAACAGATGTGACACAAATTTATTAATAATGGGAGAAATTTTGTGTATACACCG 420
 DB
 19-FEB-2004; 2004US-00781979.
 19-FEB-2004; 2004US-00782020.
 19-FEB-2004; 2004US-00782096.
 19-FEB-2004; 2004US-00782141.
 19-FEB-2004; 2004US-00782570.
 19-FEB-2004; 2004US-00783417.
 (ATHE-) ATHENIX CORP.
 Carozzi N, Harglass T, Koziel MG, Duck NB, Carr B;
 N-PSDB; ADR89396.
 WPI; 2004-635574/61.
 N-PSDB; ADR89396.
 New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 and polypeptides, useful for killing lepidopteran or coleopteran pests or
 for producing organisms with pesticide resistance.
 Claim 12; SEQ ID NO 9; 178pp; English.
 This sequence represents an isolated delta-endotoxin. Some of the delta-
 endotoxin coding sequences of the invention have alternative start
 codons, producing more than one protein from a single open reading frame.
 The nucleic acid sequences of the invention are useful in DNA constructs
 or expression cassettes for transformation and expression in plants and
 bacteria. The nucleic acids and corresponding polypeptides are useful for
 killing lepidopteran or coleopteran pests. Compositions containing the
 delta-endotoxins of the invention, and methods for their production, are
 useful for the production of organisms with pesticide resistance,
 specifically bacteria and plants. These organisms are useful for
 generating altered or improved delta-endotoxin or delta-endotoxin-
 associated proteins that have pesticidal activity, or for detecting the
 presence of delta-endotoxin or delta-endotoxin-associated proteins or
 nucleic acids in products or organisms.
 Sequence 744 AA;
 Alignment Scores:
 Pred. No.: 0 Length: 744
 Score: 3902.00 Matches: 743
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.87% Mismatches: 0
 Query Match: 99.06% Indels: 0
 DB: 8 Gaps: 0
 US-10-782-570-1 (1-2235) x ADR89397 (1-744)
 QY 1 GTGAATCAAAATAAATAATGAATATGAGATTATCGATTCAAGAATTTATCTATCCT 60
 DB 1 MetAenGlnAenAenAenAenGluTyGluileileaspSerlyAenLeuSerTyPro 20
 QY 61 TCTAACAGAAATATTGATCATCTTAGATACACCTTACACAAATAATCCAAATCAACATTA 120
 DB 21 SerAenArgAenileAenHisSerArgTyProTyThrAenAenProAenGlnProLeu 40
 QY 121 CAAACACAAATTAACAGAGTGGCTCAATGTGTCAAGGGAATACACATATGGTGAT 180
 DB 41 GlnAenThrAenTyLysGluTrpLeuAenMetCysGlnGlnTyAenThrGlnTyGlyAasp 60
 QY 181 AATTTCGAGACATTTGCTAGTGTGATACAAATTCGTCAGTGTAGTCAGGTPACTATTGTA 240
 DB 61 AenPheGluThrPheAlaSerAlaAenThrilealaalavalSerAlaGlyThrileVal 80
 QY 241 TCCGGTACTCTGTAGCCGGTATAGTGGGCTCACTTCTATATCCGGACCGGATAGGAATA 300
 DB 81 SerGlyThrLeuLeuAlaGlyileGlyGlyLeuThrSerileSerGlyProileGlyile 100
 QY 301 ATAGTGTATATAATATCTTTGGTACCTATCACTGTCITTTGGCCCGCGGGAGAA 360
 DB 101 IleGlyAlaileileileSerPheGlyThrLeuileThrValPheTrpProAlaGlyGlu 120
 QY 361 CAAGACAAAACAGATGTGACACAAATTTATTAATAATGGGAGAAATTTTGTGTATACACCG 420
 DB

Db GlnAspLysThrValTrpThrGlnPheIleLysMetGlyGluIlePheValAspThrPro 140
 QY TTAACAGAAAACATATAAAGCTTAAAGCTTACAAAGCTTTAGAGGATTTAGACAAATATTA 480
 Db LeuThrGluSerIleLysGlnLeuLysLeuGlnThrLeuGluGlyPheArgGlnIleLeu 160
 QY CAAAGCTATAATACAGCATTAGATTTGGAGAAAATTAAGAGACTACAGCTCCTCGGA 540
 Db GlnSerTyAenThrAlaLeuAaspTrpArgLysLeuLysArgLeuGlnAlaProGly 180
 QY TTACCACCATCATCAGCATTAACCAAGCTGCCTTGAATCTTAAATACGATTTGAGAAAT 600
 Db LeuProProSerSerAlaLeuGlnAlaAlaLeuThrLeuLysIleArgPheGluAen 200
 QY GTTCACAATGATTTTATTCAGAAAATACCTGGTTTCCAACTTGAACTTATAAACCGCTA 660
 Db ValHisAenAaspPheIleArgGluIleProGlyPheGlnLeuGluThrTyLysThrLeu 220
 QY TTACTACCTATTTATGCGAAGCTGCTAAATTTTCATTTAAATTTATTAACAAGGTGCT 720
 Db LeuLeuProIleTyAlaGlnAlaAlaAenPheHisLeuAenLeuGlnGlnGlyAla 240
 QY GAATTTGGCTGATGAATGGAATGAGATATACATCCTTTCAAAAATTTGAACCTTAATGCTGA 780
 Db GluLeuAlaAaspGluTrpAenAlaAaspIleHisProSerGlnIleGluProAenAlaGly 260
 QY ACATCAGATGACTATTATAAATCTTTTAAAGAAAATATACCTAAATATAGTAATCTATGT 840
 Db ThrSerAaspTyTyTyLysLeuLysLeuLysGluAenIleProLysTySerAenTyCys 280
 QY GCAAAATACCTATAGAGAGGACTAAATAACTTCGAAACGAACTTAATATGAGATGAGT 900
 Db AlaAenThrTyArgGluGlyLeuAenLysLeuAenGlnProAenMetArgTrpSer 300
 QY ATATTTAATCATTCAGAGATATATGACTATTACTGTTATGATATGATATGCTCAATTT 960
 Db IlePheAenAaspTyArgArgTyMetThrIleThrValLeuAaspThrIleAlaGlnPhe 320
 QY TCTTTTATGATATAAAGAGATACAAAGATTCATATGAGAAAGATAGTGGCATTTAAAACT 1020
 Db SerPheTyAaspIleLysArgTyLysAaspSerIleGlyArgIleGlyGlyLysThr 340
 QY GAACTTACAGAGAAATTTATACACTGAAATTAATTTTACCGCTCTTACTTACCTTTGAA 1080
 Db GluLeuThrArgGluIleTyThrThrGluIleAenPheAaspArgLeuThrTyLeuGlu 360
 QY ATTCAACCCCAATCTCGCTATAATGGAATATAATTTAAACAGCTTCAGGGCTTAGATATTT 1140
 Db IleGlnProAenLeuAlaIleMetGluTyAenLeuThrArgSerGlyLeuArgLeuPhe 380
 QY TCAATTTTAGATCACTTATATTTTATACAAAATGAAACGTCACGGGAATCGTTTAGTT 1200
 Db SerPheLeuAaspGluLeuIlePheTyThrLysAenGluThrTyGlyAenArgLeuVal 400
 QY GSTATTTCGGAATCGTAATAGATCTACTGTCACGACGAACTGAAATATATATATGGA 1260
 Db GlyIleAlaAenAargAenArgSerThrTyAlaThrThrGlyThrGluIleIleTyGly 420
 QY GAAAGAACAGGTCCACCAACAAACAACTTTTAATACCATTTCAATCTATAAAGTTTCA 1320
 Db GluArgThrGlyProProThrThrLysThrLeuIleProPheGluSerTyLysValSer 440
 QY ATTGTAACATGATAGACAGTAACCTCCTACTTCCCTTTTCCCTAACATATATTTACAAAT 1380
 Db IleValThrAaspArgGlnValThrProThrSerProPheProAenIleTyPheThrIle 460
 QY AATCAAAATGAACTTTTATTAATATTCACCTAGTAATAAATTAACATATTCAGCTGGG 1440
 Db AenGlnIleGluLeuTyLysAenAenSerProSerAenLysLeuThrTySerAlaGly 480
 QY GCGAATTTTCTAATGATAAAAACAACTGATTTTCAATTTTCTCTGTAATAAAGACTGT 1500
 Db GlyAenLeuSerAenAaspLysTyThrThrAaspPheGlnPheProValLysLysAenCys 500

QY 1501 AAACCAATTATTAATCCAAATGTTTACCAAGCTATAATAGTATAGTCAATATTTATCC 1560
 Db |||||
 QY 501 LysProIleIleAsnProAsnCysLeuProSerTyAsnSerTySerHisIleLeuSer 520
 Db |||||
 QY 1561 CAGTTTCTTATTTATTTATTTCTTATAAATTTGATTTAGGCTTAATATATATATATACA 1620
 Db |||||
 QY 521 GlnPheSerLeuPheAsnTySerTyTyIleGlyLeuAlaLeuAsnIleLeuTyThr 540
 QY 1621 GGTGCTAGTAGTACACACAGTAGTGTATATACAAATATGCAATATATGCAATATATGCAATATA 1680
 Db |||||
 QY 541 GlyAlaLeuGlyTyThrHisSerValAsnArgAsnAsnAlaIleSerAsnPlsIle 560
 Db |||||
 QY 1681 ATTCAATGATCCCAAGCAATCAAGGTAACTGTTTGTATACAAATCTTAAGGTATTTGAA 1740
 Db |||||
 QY 561 IleThrMetIleProAlaIleLysGlyAsnSerLeuAspThrAsnSerIleValIleGlu 580
 QY 1741 GGACTGTGCTATACAGAGGAAACTTGGTTTATTTTACAAAGTCAAGGGCTTTAGAGATT 1800
 Db |||||
 QY 581 GlyProGlyHisThrGlyAsnLeuValTyLeuGlnSerGlnGlyArgLeuGluIle 600
 QY 1801 ACATGTAGACTCTTAATTTTACAAATCTTATTTACATTTAGACTTCGATACGCTACAAT 1860
 Db |||||
 QY 601 ThrCysArgThrProAsnSerThrGlnSerTyTyIleArgLeuArgTyAlaThrAsn 620
 QY 1861 GGTGCTGCAATACTCTTCTTAATATATCTTACAAATACCAAGGAGTAAATAGGAATACCA 1920
 Db |||||
 QY 621 GlyAlaGlyAsnThrLeuProAsnIleSerLeuThrIleProGlyValIleGlyIlePro 640
 QY 1921 CCTCAACGACTCAACAACTTTTCTGTCACAAATATATATATATATATATATATATATATATAT 1980
 Db |||||
 QY 641 ProGlnArgLeuAsnAsnThrPheSerGlyThrAsnTyAsnAsnLeuGlnTyArgIleAsp 660
 QY 1981 TTTGGGTATTTCCATTTCCAGTACAGTACATTTACCTTTAAATCGAAACATACATTT 2040
 Db |||||
 QY 661 PheGlyTyThrPheGlnPheProSerThrValThrLeuProLeuAsnArgAsnIleProPhe 680
 QY 2041 ATATTATTCGTCAGATGTATCAATTTCAATTTTATTTATTTATTTATTTATTTATTTATTTAT 2100
 Db |||||
 QY 681 IlePheAsnArgAlaAspValSerAsnSerIleLeuIleAspIleValIleGluPheIle 700
 QY 2101 CCAATTACTCTCTGTAGCCCAATATAGAGAAAACAAATTTAGAACTATCCAAACA 2160
 Db |||||
 QY 701 ProIleThrSerSerValArgGlnAsnArgGluLysGlnLysLeuGluThrIleGlnThr 720
 QY 2161 AAAATATATATATTTTCAATTCATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 2220
 Db |||||
 QY 721 LysIleAsnThrPhePheThrAsnHisThrTyAsnThrLeuAsnIleGluAlaThrAsn 740
 QY 2221 TATGATATTGAT 2232
 Db |||||
 QY 741 TyrAspIleAsp 744

RESULT 2

ADR89399
 ID ADR89399 standard; protein; 694 AA.
 XX AC ADR89399;
 XX DB ADR89399;
 DT 18-NOV-2004 (first entry)
 DE AXMI-007 alternative protein.
 XX KW delta-endotoxin; delta-endotoxin in associate polypeptide;
 KW expression cassette; transformation; transgenic; plant; bacteria;
 KW lepidoptera; coleoptera; pest; pesticide; resistance;
 KW pesticidal activity.
 XX OS Bacillus thuringiensis.
 XX FN WO2004074462-A2.
 XX DB 02-SEP-2004.
 QY 151 ATGTCGTCAGGATACACAAATATGTCATATTTTCGAGACATTTGCTAGTCTGATACA 210
 Db |||||
 QY 1 MetCysGlnGlyAsnThrGlnTyArgIleAsnPheGluThrPheAlaSerAlaAspThr 20
 QY 211 ATTCGTCAGGATGTCAGGATCTATTTGCTATCCGCTACTCTGTTAGCCGTTATAGTGGG 270
 Db |||||
 QY 21 IleAlaIleValSerAlaGlyThrIleValSerGlyThrLeuLeuAlaGlyIleGlyGly 40
 QY 271 CTCATCTTATATCCGACCGGATAGGATATAGTCTATATATATATATATATATATATATAT 330
 Db |||||
 QY 41 LeuThrSerIleSerGlyProIleGlyIleIleGlyAlaIleIleSerPheGlyThr 60
 QY 331 CTAATCAGTCTTTTGGCCGCGGAGAAACAAAGACAAAGATGATGACACAAATTTAT 390
 Db |||||
 QY 61 LeuIleThrValPheThrProAlaGlyGluGlnAspLysThrValThrThrGlnPheIle 80
 QY 391 AAAATGGGAGAAATTTTGTGTATACACCGTTTAAACAGAAACATAAACACAGTAAAGTTA 450

XX 20-FEB-2004; 2004WO-US005829.
 XX PF 20-FEB-2003; 2003US-0448632P.
 XX PR 20-FEB-2003; 2003US-0448633P.
 XX PR 20-FEB-2003; 2003US-0448737P.
 XX PR 20-FEB-2003; 2003US-0448806P.
 XX PR 20-FEB-2003; 2003US-0448810P.
 XX PR 20-FEB-2003; 2003US-0448812P.
 XX PR 19-FEB-2004; 2004US-00781979.
 XX PR 19-FEB-2004; 2004US-00782020.
 XX PR 19-FEB-2004; 2004US-00782096.
 XX PR 19-FEB-2004; 2004US-00782141.
 XX PR 19-FEB-2004; 2004US-00782570.
 XX PR 19-FEB-2004; 2004US-00783417.
 XX PA (ATHE-) ATHENIX CORP.
 XX FI Carozzi N, Hargiss T, Kozziel MG, Duck NB, Carr B;
 XX WI; 2004-635574/61.
 XX N-PSDB; ADR89398.
 DR WPI; 2004-635574/61.
 XX N-PSDB; ADR89398.
 DR New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 XX and polypeptides, useful for killing lepidopteran or coleopteran pests or
 XX for producing organisms with pesticide resistance.
 PT Claim 12; SEQ ID NO 11; 178pp; English.
 PS This sequence represents an isolated delta-endotoxin. Some of the delta-
 XX endotoxin coding sequences of the invention have alternative start
 CC codons, producing more than one protein from a single open reading frame.
 CC The nucleic acid sequences of the invention are useful in DNA constructs
 CC or expression cassettes for transformation and expression in plants and
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for
 CC killing lepidopteran or coleopteran pests. Compositions containing the
 CC delta-endotoxins of the invention, and methods for their production, are
 CC useful for the production of organisms with pesticide resistance,
 CC specifically bacteria and plants. These organisms are useful for
 CC generating altered or improved delta-endotoxin or delta-endotoxin-
 CC associated proteins that have pesticidal activity, or for detecting the
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
 CC nucleic acids in products or organisms.
 XX Sequence 694 AA;
 SQ

Alignment Scores:
 Pred. No.: 1.37e-296 Length: 694
 Score: 3623.00 Matches: 694
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 91.98% Indels: 0
 DB: Gaps: 0

US-10-782-570-1 (1-2235) x ADR89399 (1-694)

Db 81 LysMetGlyGluLeuPheValAspThrProLeuThrGluSerIleLysGlnLeuLysLeu 100
QY 451 CAACTTTAGAGGATTTAGACAAATATTAACAAGCTATATACAGCATTAAGATGAG 510
Db 101 GlnThrLeuGluGlyPheArgGlnIleLeuGlnSerTyrAsnThrAlaLeuAspAspTrp 120
QY 511 AGAAATTAAGAAAGACTCAAGCTCTCGATTACCAACCATCATCAGCATTTACAACAAGCT 570
Db 121 ArgLysLeuLysArgLeuGlnAlaProGlyLeuProProSerSerAlaLeuGlnGlnAla 140
QY 571 GCCTTGACTCTTAAATAGATTGAGAAATGTCACAATGATTTATTCGAGAAATACCT 630
Db 141 AlaLeuThrLeuLysIleArgPheGluAsnValHisAsnAspPheIleArgGluIlePro 160
QY 631 GGTTCCTCAACTGAAACTTATAAAGCTGATTTACTTACTTATTTATGCGCAAGCTGCTAAT 690
Db 161 GlyPheGlnLeuGluThrTyrLysThrLeuLeuLeuProIleTyrAlaGlnAlaAlaAsn 180
QY 691 TTTCAATTTAAATTTATTACAACAGGTCTGAAATGGCTGATGAATGGAATGCAGATATA 750
Db 181 PheHisLeuAsnLeuLeuGlnGlnGlyAlaGluLeuAlaAspGluTrpAsnAlaAspIle 200
QY 751 CATCTTCACAAATGAACCTTAATGCTGGAAATCAGATGACTATATATAACTTTTAAAA 810
Db 201 HisProSerGlnIleGluProAsnAlaGlyThrSerAspAspTyrTyrLysLeuLys 220
QY 811 GAAATATACCTTAATATAGTAATCTATGTCGAATACCTATAGAGAGGCTTAATAAA 870
Db 221 GluAsnIleProLysTyrSerAsnTyrCysAlaAsnThrTyrArgGluGlyLeuAsnLys 240
QY 871 CTTCGAAACGAACTTAATATGAGATGAGTATATTAATGATTAATCGAAGATATATGACT 930
Db 241 LeuArgAsnGluProAsnMetArgTrpSerIlePheAsnAspTyrArgArgTyrMetThr 260
QY 931 ATTACTGATTAGATCTATCGCTCAATTTCTTTTATGATATATAAGAGATACAAAGAT 990
Db 261 IleThrValLeuAspThrIleAlaGlnPheSerPheTyrAspIleLysArgTyrLysAsp 280
QY 991 TCATATAGCAAGATAGGCGCATTAACCTCAACTTCAAGCAAGAAATTTATCAACTGAA 1050
Db 281 SerIleGlyArgIleGlyIleLysThrGluLeuThrArgGluIleTyrThrThrGlu 300
QY 1051 ATAAATTTGACCGCTTACTTACCTCGAAATTCACCCCAATCTCGCTATATATGCAATAT 1110
Db 301 IleAsnPheAspArgLeuThrTyrLeuGluIleGlnProAsnLeuAlaIleLeuGluTyr 320
QY 1111 AATTTAACAGCTTCAGGCTTAGATTTATTTCAATTTTAGATGAACTTATATTTTATACA 1170
Db 321 AsnLeuThrArgSerGlyLeuArgLeuPheSerPheLeuAspGluLeuIlePheTyrThr 340
QY 1171 AAAATGAAAGCTACGGGAATCGTTAGTTGGTATTCGGAATCGTAATAGATCTACTTAT 1230
Db 341 LysAsnGluThrTyrGlyAsnArgLeuValGlyIleAlaAsnArgAsnArgSerThrTyr 360
QY 1231 GCTACGACAGAACTGAAATTTATATCGGAAAGAACAGGTCCACCCACACAAACAAACT 1290
Db 361 AlaThrThrGlyThrGluIleIleTyrGlyGluArgThrGlyProProThrThrLysThr 380
QY 1291 TTAATACCATTTGAATCTTATAAAGTTTCAATTTGATGATAGACAGTAACTCTTACT 1350
Db 381 LeuIleProPheGluSerTyrLysValSerIleValThrAspArgGlnValThrProThr 400
QY 1351 TCCCTCTTTCTACATATATCTTACATTTAATCAATTTGAACTTTATTTAAATTAATCA 1410
Db 401 SerProPheProAsnIleTyrPheThrIleAsnGlnIleGluLeuTyrLeuAsnAsnSer 420
QY 1411 CCTAGTAAATAATAACATATTTAGCTGGGGGAATTTATCTAATGATATAAAAAACAACT 1470
Db 421 ProSerAsnLysLeuThrTyrSerAlaGlyAsnLeuSerAsnAspLysLysThrThr 440
QY 1471 GATTTTCAATTTCTGTAAAAAGACTGTAAACCAATTTATTAATCCAAATTTGTTACCA 1530

Db 441 AspPheGlnPheProValLysLysAspCysLysProIleAsnProAsnCysLeuPro 460
QY 1531 AGCTATATATAGTTATAGTATATATTTATCCAGTTTCTTTATTAATTTCTCTATAAA 1590
Db 461 SerTyrAsnSerTyrSerHisIleLeuSerGlnPheSerLeuPheAsnTyrSerTyrLys 480
QY 1591 ATTGGAATTAGCGCTAAATATATATATATACAGGTGCATTAGGATCGACACACAGTAGTGT 1650
Db 481 IleGlyLeuAlaLeuAsnIleLeuTyrThrGlyAlaLeuGlyTyrThrHisSerSerVal 500
QY 1651 AATGAAATTAATGCAATATCAGATAAAATTAATTAATGATCCAGCAATCAAAAGGTAAAC 1710
Db 501 AsnArgAsnAsnAlaIleSerAspLysIleIleThrMetIleProAlaIleLysGlyAsn 520
QY 1711 AGTCTTCATCAAACTCTAAGGTAAATTAAGAGGCTCGTTCATACAGGAGAACTTGTGT 1770
Db 521 SerLeuAspThrAsnSerLysValIleGluGlyProGlyHisThrGlyGlyAsnLeuVal 540
QY 1771 TATTTACAAAGTCAAGGCGCTTTAGAGATTAATCATGTAGAACTCTTAATTTTACACAATCT 1830
Db 541 TyrLeuGlnSerGlnGlyArgLeuGluIleThrCysArgThrProAsnSerThrGlnSer 560
QY 1831 TATTAATGATGATTCGATACGCTACAAATGGTCTCGAAATACTCTTCTTAATATATCT 1890
Db 561 TyrTyrIleArgLeuArgTyrAlaThrAsnGlyAlaGlyAsnThrLeuProAsnIleSer 580
QY 1891 CTTACATACACGAGGATTAAGGAATACCACTCAACGACTCAACACACTTTTCTCTCGT 1950
Db 581 LeuThrIleProGlyValIleGlyIleProProGlnArgLeuAsnAsnThrPheSerGly 600
QY 1951 ACAATTAATTAATTAATTAATACGAGATTTTGGGTATTTTCCAATTTTCCAAGTACAGTA 2010
Db 601 ThrAsnTyrAsnAsnLeuGlnTyrGlyAspPheGlyTyrPheGlnPheProSerThrVal 620
QY 2011 ACATTACTTTAAATCGAAACATACATCAATTTATTTAATCGTGAGATGATCAAAATCA 2070
Db 621 ThrLeuProLeuAsnArgAsnIleProPheIlePheAsnArgAlaAspValSerAsnSer 640
QY 2071 ATTTTAATCATGTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2130
Db 641 IleLeuIleIleAspLysIleGluPheIleProIleThrSerSerValArgGlnAsnArg 660
QY 2131 GAAAAACAAAAATTAGAACTATCCAAACAAAAATAAATACATTTTTCACAAATCATACA 2190
Db 661 GluLysGlnLysLeuGluThrIleGlnThrLysIleAsnThrPhePheThrAsnHisThr 680
QY 2191 AAAATACTTTTAAATATAGAACCAACAACTATGATATTGAT 2232
Db 681 LysAsnThrLeuAsnIleGluAlaThrAsnTyrAspIleAsp 694
RESULT 3
ADR89395
ID ADR89395 standard; protein; 735 AA.
XX AC
XX ADR89395;
DT 18-NOV-2004 (first entry)
XX DE AXMI-006.
XX KW delta-endotoxin; delta-endotoxin associate polypeptide;
XX KW expression cassette; transfection; transgenic; plant; bacteria;
XX KW lepidoptera; coleoptera; pest; pesticide; resistance;
XX KW pesticidal activity.
XX OS Bacillus thuringiensis.
XX PN WO2004074462-A2.
XX PD 02-SEP-2004.
XX PF 20-FEB-2004; 2004WO-US005829.
XX

Db 460 PheIleIleAenGlnIleGluLeuTyrlLeuAenGlySerAenAenThrlLeuLyTy 479
 Qy 1432 TCAGCTGGGGGAATTTATCTAATGATATAAAACAACTGATTTTCAATTTCTCGTAA 1491
 Db 480 SerAlaGlyGlySerLeuSerAenTyrgLnaenThrPhePheGlnPheProArgLy 499
 Qy 1492 AAAGACTGTAAACCAATTATTAATCCAAATGTTTACCAGCTATAATAGTATAGTCAT 1551
 Db 500 LysAepCyAenAenLeuValIleAepProGlyCyBserProAenPheAenAenTySerHis 519
 Qy 1552 ATTTTATCCAGTTTCTTTATTTAATTTATCTTATAAAATTTGGATTAGCGCTAAATATA 1611
 Db 520 IleLeuSerHisPheSerLeuPheThrTySerTyValIleGlyLeuGlnLeuGlnIle 539
 Qy 1612 TTATATACAGGTGCATTTAGATGGACACACAGTAGTGTATAAGAAATTAATGCAATATCA 1671
 Db 540 LeuAepThrGlyValLeuGlyTrpThrHisSerSerValAepArgTyAenAlaIleSer 559
 Qy 1672 GATAAAATTAATTACAAATGCCAGCAATCCAGTAACTGATCACTCTGTACAACTCTAAG 1731
 Db 560 AspyIleIleThrMetIleProAlaIleGlyAenAenLeuAepThrAenSerLy 579
 Qy 1732 GTAATTGAAGACCTGGTCATACAGAGGAACTTTGGTTTATTTACAAAGTCAAGGGCGT 1791
 Db 580 ValIleGluGlyProGlyHisThrGlyAenLeuValTyLeuGlnSerGlnGlyArg 599
 Qy 1792 TTAGAGATTACATGTAGAACTCTTAATTTCTACAACTCTTATTAATACATAGACTCGATAC 1851
 Db 600 LeuGluIleThrCysGluThrProAenSerThrGlnSerTyPheIleArgLeuArgTy 619
 Qy 1852 GCTCAAAATGGTGGAAATCTCTCTAATATCTCTTACAACTACAGGAGTAAATA 1911
 Db 620 AlaThrAenGlyAlaGlyAenThrLeuProAenIleSerLeuThrIleProGlyValIle 639
 Qy 1912 GGAATPACCACTCAACGACTCAACAACTCTTTCTGCTACAAATTAATAATTTACAA 1971
 Db 640 GlyIleProGlnArgLeuAenAenThrPheSerGlyThrAenTyAenAenLeuGln 659
 Qy 1972 TACGAGATTTGGGTATTTCCAAATTTCCAAAGTACAGTAACTACCTTTAAATCGAAAC 2031
 Db 660 TyrGlyAepPheGlyTyPheGlnPheProSerThrValThrLeuProLeuAenArgAen 679
 Qy 2032 ATACATTTATTTAATTCGTCAGATGTATCAATTCATCAATTTAATCAATTTGATAAAT 2091
 Db 680 IleProPheIlePheAenArgAlaAepValSerAenSerIleLeuIleAepLy 699
 Qy 2092 GAATTTATACCAATTTACTCTCTGTAGCCCAAAATAGAGAAAAACAAATTTAGAACT 2151
 Db 700 GluPheIleProIleThrSerSerMetHisGlnAenArgGluLyGlnLyLeuGluThr 719
 Qy 2152 ATCCMAACAAAATAATACATTTTTCACAAATCAATACAAA 2193
 Db 720 IleGlnThrLyIleAenThrPhePheThrAenHisThrLy 733

RESULT 4

AAP93715
 ID AAP93715 standard; protein; 1180 AA.
 XX
 AC AAP93715;
 DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 30-MAY-1990 (first entry)
 XX
 DE Delta-endotoxin crystal protein.
 XX
 KW Delta-endotoxin; crystal protein; insecticide; biological control agent;
 KW PCH130.
 OS Bacillus thuringiensis: israelensis.
 XX
 PN EP296870-A.

XX 28-DEC-1988.
 PD
 XX 24-JUN-1988; 88EP-00305772.
 PF
 XX 26-JUN-1987; 87US-00067653.
 PR
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA
 XX Eller DJ, Ward ES;
 FI WPI; 1989-001322/01.
 XX N-PSDB; AAN93059.
 DR
 XX DNA fragment encoding insecticidal protein - obtd. from Bacillus
 PT thuringiensis sub species israelensis, and used in microorganisms and
 PT plant cells.
 XX
 PS Disclosure; Page: 26pp; English.
 PS The 130 kDa delta-endotoxin from B. thuringiensis subsp. israelensis is
 CC encoded by a 4.46 kb insert of pCH130. The protein is insecticidal and
 CC can be used to control insect pests esp. mosquitos. See also AAP94035.
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to
 CC correct OS field.)
 XX
 SQ Sequence 1180 AA;
 Alignment Scores:
 Pred. No.: 1.14e-88 Length: 1180
 Score: 1159.00 Matches: 283
 Percent Similarity: 54.55% Conservative: 131
 Best Local Similarity: 37.29% Mismatches: 281
 Query Match: 29.42% Indels: 64
 DB: Gaps: 25
 US-10-782-570-1 (1-2235) x AAP93715 (1-1180)

Qy 13 ANTAATTAATGAATGATGATTATCGATTCA-----AAGAAATTTATCTTATCTCTTAAC 66
 Db 6 AsnLyAenGluTyrgLnaenThrLeuAenAlaSerGlnLyAenLeuAenIleSerAenAen 25
 Qy 67 AGAAATATTGATCATCTAGATACCTTTACACAAATTAATCCAAATCAACCAATCAACAAAC 126
 Db 26 -----TyrThrArgTyrgLnaenSerProLyGlnLeuLeuGlnSer 41
 Qy 127 ACAAATTAACAAAGAGTGGCTCAATATGTGTCAAGGGAATACAAATATGGTGAATAATTC 186
 Db 42 ThrAenTyrgLyAepTrpLeuAenMetCysGlnGlnAenGlnTyrgLyGlyAepPhe 61
 Qy 187 GAGACATTTGCTAGTCTGATACAAATGCTGTCAGATTAGTCAGGTACTATTGTATCCGGT 246
 Db 62 GluThrPheIleAepSer-----GlyGluLeuSerAlaTyThrIleValIleValGly 78
 Qy 247 ACTCTGTTAGCGGTATAGTGGCTCCTCTATATATCCGACCGATAGGAATAATAGGT 306
 Db 79 ThrValLeuThrglyPheGlyPheThr-----ProLeuGlyLeu----- 92
 Qy 307 GCTATAATAATATCTTTTGTACCTTAATCACTGTCTTTTGGCCCGGGAGAACAAAGAC 366
 Db 93 ---AlaLeuIleGlyPheGlyThrLeuIleProValLeuPheProAlaGlnAepGlnSer 111
 Qy 367 AAACAGTATGGACACAAATTTATAAATGGGAGAAATTTTGTGTGTATACACCTTAAACA 426
 Db 112 AsnThr---TrpSerAepPheIleThrGlnThrLyAenIleIleLyAenGluIleAla 130
 Qy 427 GAAGACATAAACAGCTAAAGTTTACAACTTTAGAACGATTAGACAAATATTAACAAGC 486
 Db 131 SerThrTyrgLySerAenAlaAenLyIleLeuAenArgSerPheAenValIleSerThr 150
 Qy 487 TATAATAACAGCATTTAGATGTTGGAGAAAATTAAGAAAGACTACAAAGCTCTCGATTACCA 546
 Db 151 TyrHisAenHisLeuLySerThrTrpGlu-----AenAenProAenProGln 165

QY 547 CCATCATCAGCATACAAAGCTGCCTTGAATCTTAAATAACGATTTGGAATGTCAC 606
Db 166 AsnThrGlnAspValAlaThrGlnGlnLeuValHisTyrHisPheGlnAsnValIle 185
QY 607 AATGATTTTATTCAGGAATACCT-----GGTTTCCAACTTGAACCTTATAAAGCTA 660
Db 186 ProGluLeuValAsnSerCysProProAsnProSerAspCysAspTyrTyrAsnIleLeu 205
QY 661 TTACTACCTATTATGCGCAAGCTGCTTAATTTTCAATTTTAAATTTATTAACAAGGCTCT 720
Db 206 ValLeuSerSerTyrAlaGlnAlaAlaAsnLeuHisLeuThrValLeuAsnGlnAlaVal 225
QY 721 GAATTTGGCTGATGAATGCGAGATATACATCTCTTCAAAATTTGAACCTTAATGCTGGA 780
Db 226 LysPheGluAlaTyrLeuLysAsnAsnArgGlnPheAspTyrLeuGluPro---LeuPro 244
QY 781 ACATCAGATGACTATTATAAACTTTTAAAGAAATATACCTAAATATAGTAATCTATTGT 840
Db 245 ThrAlaIleAspTyrTyrProValLeuThrLysAlaIleGluAspTyrThrAsnTyrCys 264
QY 841 GCAATACCTATAGAGAAGGCTAAATAAATCTTGAACGAACT----- 885
Db 265 ValThrTyrLysLysGlyLeuAsnLeuIleLysThrThrProAspSerAsnLeuAsp 284
QY 886 ---AATATGATGAGCTATATTATTAATGATTCGAGATATATGACTATTACTGTATTA 942
Db 285 GlyAsnIleAsnThrPheAsnThrTyrAsnThrTyrArgThrLysMetThrAlaValLeu 304
QY 943 GATACATTCGCTCAATTTCTTTTATGATATAAGAGATACAAAGATTCATAGGAAGA 1002
Db 305 AspValValAlaLeuPheProAsnTyrAspValGlyLysTyrProIle----- 320
QY 1003 ATAGTGGCATTAACCTGAATTAACAGAAATTTATACACTGAATAAATTTGAC 1062
Db 321 ----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal---LeuAsnPheGlu 337
QY 1063 GCTCTTACTACCTGAAATTCACCCCAATCTCGCTAATGGAATATAATTTAACAGCT 1122
Db 338 GluSerProTyrLysTyrTyr-----AspPheGlnTyrGlnGluAspSerLeuThrArg 355
QY 1123 TCAGGCTTAGATTTTATGATGAACCTTATATTTATACAAAATAAAGAAACG 1182
Db 356 ArgPro---HisLeuPheThrTrpLeuAspSerLeuAsnPheTyrGluLysAlaGlnThr 374
QY 1183 TAGCGGAATCGTTAGTTGGTATTCGGAATCGTAATAGATCTACTTATGCT----- 1233
Db 375 ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn 393
QY 1234 ACGCAGGAATCGAATTTATATATGGAAGAAAGACAGCTCCACCACAAACAACTTTA 1293
Db 394 IleSerGlnLysSerSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu 413
QY 1294 ATACCATTTGAATCTATAAAGTTTCAATTTGTAATGTAGTAGCAAGTACTCTACTTCC 1353
Db 414 -----GlyLeuAlaThrAsnIleTyrIlePheLeuLeuAsnValIleSerLeuAspAsn 431
QY 1354 CTTTTCCTAATATATTTTACAAATTAATCAAAATGAACTTTTAAATAATTAATTCACCT 1413
Db 432 LysTyrLeuAsnAspTyrAsnAsnIleSerLysMetAspPheIleThrAsnGlyThr 451
QY 1414 -----AGTAATAATTAACATTTATTCAGCTGGGGGAATTTATCTAATGATAAAAA 1464
Db 452 ArgLeuLeuGluLysGluLeuThr---AlaGlySerGlyGlnIleThrTyrAspValAsn 470
QY 1465 ACAACCTGATTTTCAATTTCTGTAAAAAGAGCTGTAAACCAATTTATTAATCCAAATGT 1524
Db 471 LysAsnIlePheGlyLeuProIleLeuLysArgArgGluAsnGlnGlyAsnProThrLeu 490
QY 1525 TTACCAAGCTAATAATAGTTATAGTGCATATTTTATCCAGGTTTCTTTTATTTAATAT --- 1581
Db 491 PheProThrTyrAspAsnTyrSerHisIleLeuSerPheIleLysSerLeuSerIlePro 510

QY 1582 ---TCCTATAAAATTTGGATTAGCGCTAAATATATATATATATATATATATAGGATGGACA 1638
Db 511 AlaThrTyrLys-----ThrGlnValTyrThrPheAla-----TrpThr 523
QY 1639 CACAGTAGTTAATAGAAATAATGCAATATCAGATAAATAATTAATATATATATATATATAT 1698
Db 524 HisSerValAspProLysAsnThrIleTyrThrHisLeuThrThrGlnIleProAla 543
QY 1699 ATCAAAAGTAACTCTTGATACAACTCTTAAGGTAATTAAGGAGCTGTCATACAGGA 1758
Db 544 ValLysAlaAsnSerLeuGlyThrAlaSerLysValValGlnGlyProGlyHisThrGly 563
QY 1759 GGAACCTTGGTTTATTACAAAGTCAAGGGCTTTAGAGATTCATATGATAGAACCTCTAAT 1818
Db 564 GlyAspLeuIle-----AspPheLysAsnHisPheLysIleThrCysGlnHisSerAsn 581
QY 1819 TCTACAACTTTATACATTAGACTTCGATACCTACAAATGCTGCTGGAATAATCTCTT 1878
Db 582 PheGlnGlnSerTyrPheIleArgTyrAlaSerAsnGlySerAlaAsnThrArg 601
QY 1879 CCTAATATATCTCTCAATACACAGGAGTATAGTAATACCACTCAACGACTCAACAC 1938
Db 602 AlaValIleAsnLeuSerIleProGlyValAlaGluLeu---GlyMetAlaLeuAsnPro 620
QY 1939 ACTTTTCTGTCACAAATTAATAATTTACAAATACGAGATTTTGGGTATTTCCAAATTT 1998
Db 621 ThrPheSerGlyThrAspTyrThrAsnLeuLysTyrLysAspPheGlnTyrLeuGluPhe 640
QY 1999 CCAATGACGATACATACCTTTTAAATCGAAACATACCATTTATATTTAATTCGTCAGAT 2058
Db 641 SerAsnGluValLysPheAlaProAsnGlnAsnIleSerLeuValPheAsnArgSerAsp 660
QY 2059 GTA---TCAAATTCATTTTAAATTCATGATAAATAATTAATTAATTAATTAATTAAT 2115
Db 661 ValTyrThrAsnThrThrValLeuIleAspLysIleGluPheLeuProIleThrArgSer 680
QY 2116 GTACGCCAAATAGAGAAAACAAATAATTAAGAACTATCCAAACAAATAAATAATACATTT 2175
Db 681 IleArgGluAspArgGluLysGlnLysLeuThrValGlnGlnIleIleAsnThrPhe 700
QY 2176 TTCCAATCATACAAATAATCTTTAAATATAGAACCCACAACTATGATATATGAT 2232
Db 701 TyrAlaAsnProIleLysAsnThrLeuGlnSerGluLeuThrAspTyrAspIleAsp 719
RESULT 5
ADR89426
ID ADR89426 standard; protein; 1180 AA.
AC ADR89426;
XX
XX 18-NOV-2004 (first entry)
DT
XX
DE cry4Aa.
XX
XX delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; pest; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
XX pestifical activity.
OS
XX Bacillus thuringiensis.
XX
XX WO2004074462-A2.
XX
XX 02-SEP-2004.
XX
XX 20-FEB-2004; 2004WO-US005829.
XX
XX 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.

Db 265 ValThrThrThrLysLysGlyLeuAsnLeuIleLysThrThrProAspSerAsnLeuAsp 284
Qy 886 ---AATATGAGATGGAGTATATTAATGATATCGAGATATGACATTAATGATGATTA 942
Db 285 GlyAsnIleAsnThrPAsnThrLysAsnThrLysArgThrLysMetThrAlaValLeu 304
Qy 943 GATACATCGCTCAATTTCTTTTATGATATAAGAGATACAAAGATTCATAGGAAGA 1002
Db 305 AspLeuValAlaLeuPheProAsnTyrAspValGlyLysTyrProIle----- 320
Qy 1003 ATAGTGGCATTAACACTGAACCTACAGAGAAATTTATACACTGAAATTAATTTGAC 1062
Db 321 -----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal---LeuAsnPheGlu 337
Qy 1063 CGTCTTACTTACTTGAATTCACCCCAATCTCGCTATAATGGAATATAATTTAACAGT 1122
Db 338 GluSerProTyrLysTyrTyr-----AspPheGlnTyrGlnGluAspSerLeuThrArg 355
Qy 1123 TCAGGGCTTAGATATTTTCAATTTTAGATGAACCTTATATTTATACAAAAAATGAACG 1182
Db 356 ArgPro---HisLeuPheThrTrpLeuAspSerLeuAsnPheTyrGluLysAlaGlnThr 374
Qy 1183 TAGCGGAATCGTTAGTGGTATTCGGAATCGTAAATAGATCTACTTATGCT----- 1233
Db 375 ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn 393
Qy 1234 ACGACAGGAACGAAATTTATATATGAGAGAAAGACAGCTCCACCAACAAACAACTTGA 1293
Db 394 IleSerGlnLysSerSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu 413
Qy 1294 ATACCAATTTGAATCTTATAAAGATTCGAATTTGTAATGATAGACAACTCTACTTCC 1353
Db 414 -----GlyLeuAlaThrAsnIleTyrIlePheLeuLeuAsnValIleSerLeuAspAsn 431
Qy 1354 CCTTTCCTACATATCTTTACAAATTAATCAAAATGAACCTTATTTAAATAATTCACCT 1413
Db 432 LysTyrLeuAsnAspTyrAsnAsnIleSerLysMetAspPheIleThrAsnGlyThr 451
Qy 1414 -----AGTAATAATTAACATATTCAGCTGGGGGAATTTATCTAATGATATAAAAA 1464
Db 452 ArgLeuLeuGluLysGluLeuThr---AlaGlySerGlyGlnIleThrTyrAspValAsn 470
Qy 1465 ACAACTGATTTCAATTTCTGTAATAAAGAACTGTAAACCAATTTATTAATCCAAATGT 1524
Db 471 LysAsnIlePheGlyLeuProIleLeuLysProArgGluAsnGlnAlaIleProThrLeu 490
Qy 1525 TTACCACTATAATAGTATAGTATATTTATCCAGTTTCTCTTTATTAATATAT--- 1581
Db 491 PheProThrTyrAspAsnTyrSerHisIleLeuSerPheIleLysSerLeuSerIlePro 510
Qy 1582 ---TCCTATAAATTTGGATTAGCGCTAAATATATATATATATACAGGTGCTAGGATGACA 1638
Db 511 AlaThrTyrLys-----ThrGlnValTyrThrPheAla-----TrpThr 523
Qy 1639 CACAGTAGTGTAAATAGAAATAATGCAATATCAGATAAATAATTAATGATCCAGCA 1698
Db 524 HisSerSerValAspProLysAsnThrIleTyrThrHisLeuThrThrGlnIleProAla 543
Qy 1699 ATCAAAGGTAACAGCTTTGATACAAACTCTAAGGTAATTAAGAGACCTGGTCATACAGA 1758
Db 544 ValLysAlaAsnSerLeuGlyThrAlaSerLysValValGlnGlyProGlyHisThrGly 563
Qy 1759 GGAACCTGGTTTATTAACAAGTCAGGGCGGTTTAGAGATTACATGATAGAACTCTAAT 1818
Db 564 GlyAspLeuIle-----AspPheLysAspHisPheLysIleThrCysGlnHisSerAsn 581
Qy 1819 TCTACACATCTTATTAACATAGCTTCGATCGCTACAAATGGTGGTGAATACTCTT 1878
Db 582 PheGlnGlnSerTyrPheIleArgIleArgTyrAlaSerAsnGlySerAlaAsnThrArg 601
Qy 1879 CCTAATATATCTTTACATATACAGGAGTAATAGGAATACCACTCAACGATCTCAACAC 1938
Db 602 AlaValIleAsnLeuSerIleProGlyValAlaGluLeu---GlyMetAlaLeuAsnPro 620

Qy 1939 ACTTTTCTGTACAAATATATAATTAATTAACATACGAGATTTTGGTATTTTCCAATTT 1998
Db 621 ThrPheSerGlyThrAspTyrThrAsnLeuLysTyrLysAspPheGlnTyrLeuGluPhe 640
Qy 1999 CCAAGTACAGTAACATTTACCTTTAAATCGAAACATACCATTTATATTAATCGTCAGAT 2058
Db 641 SerAsnGluValLysPheAlaProAsnGlnAsnIleSerLeuValPheAsnArgSerAsp 660
Qy 2059 GTA---TCAAAATCAATTTTAATCATTTGATAAAATTTGAATTTATATACCAATTTCTCTCT 2115
Db 661 ValTyrThrAsnThrThrValLeuIleAspLysIleGluPheLeuProIleThrArgSer 680
Qy 2116 GTAGCCAAATAGAGAAACAAAAATTTGAAACTATCCAAACAAAAATAATATACATTT 2175
Db 681 IleArgGluAspArgGluLysGlnLysLeuGluThrValGlnGlnIleAsnThrPhe 700
Qy 2176 TTCACAAATCATACAAAAATACCTTTAAATATAGAACCAAACTATGATATTTGAT 2232
Db 701 TyrAlaAsnProIleLysAsnThrLeuGlnSerGluLeuThrAspTyrAspIleAsp 719

RESULT 9

AAR63078
ID AAR63078 standard; protein; 1180 AA.

XX
AC AAR63078;

XX
DT 25-MAR-2003 (revised)

XX
DT 12-AUG-1995 (first entry)

XX
DE B.T. toxin PS71M3.

XX
KW Delta-endotoxin; crystal protein; biological control agent; Calliphoridae;
KW screw-worm; sheep blowfly; Lucilia; Phormia; Calliphora; insecticide;
XX pesticide; B.t.

XX
OS Bacillus thuringiensis.

XX
PN W09502694-A2.

XX
PD 26-JAN-1995.

XX
PF 13-JUL-1994; 94WO-US007902.

XX
PR 15-JUL-1993; 93US-00093199.

XX
PA (MYCO) MYCOGEN CORP.

XX
PI Hickie LA, Payne J;

XX
DR WPI, 1995-067338/09.

XX
DR N-PSDB; AAQ81178.

XX
PT Method for controlling Calliphoridae pests - specifically utilises
PT Bacillus thuringiensis isolates or toxins.

XX
PS Disclosure; Page 36-38; 50pp; English.

XX
CC A library was constructed from Bacillus thuringiensis PS71M3 total
CC cellular DNA in lambda Gem-11. Plasmid pMYC1625, selected in Escherichia
CC coli, contained a 8.0 kb insert expressing a beta-endotoxin gene. This
CC was sequenced (AAQ81178). A cured, acrycaltiferous B.t. host carrying
CC pMYC1625 produced a 130 kDa crystal protein (AAR63078) toxic to
CC calliphorids. (Updated on 25-MAR-2003 to correct PN field.)

XX
SQ Sequence 1180 AA;

Alignment Scores:

Pred. No.:	3,64e-88	Length:	1180
Score:	1153.00	Matches:	282
Percent Similarity:	54.41%	Conservative:	131
Best Local Similarity:	37.15%	Mismatches:	282
Query Match:	29.27%	Indels:	64

DB: 2 Gaps: 25

US-10-782-570-1 (1-2235) x AAR63078 (1-1180)

Qy 13 AATAAATGAATATGAGTATTCGATTCA-----AGAATTATCTTATCCTTCTTAAC 66
||| ||| ||| ||| : : : : : ||| ||| : : : : :
Db 6 AsnLysAsnGluTyrgluthrLeuAsnAlaSerGlnLysLysLeuAsnIleSerAsnAsn 25
:
Qy 67 AGAAATATTGATCATCTTAGATACCCTTACACAATAATCCAAATCAACCATTTACAAAAC 126
: : : : : ||| ||| : : : : : ||| ||| : : : : :
Db 26 -----TyrThrArgTyPProIleGluAsnSerProLysGlnLeuLeuGlnSer 41
:
Qy 127 ACAAAATTACAAAGAGTGCTCAATATGTGTACGGGAATACACAATATGTGATTAATTC 186
||| ||| ||| ||| : : : : : ||| ||| : : : : :
Db 42 ThrAsnTyrlsAspTlpLeuAsnMetCysGlnGlnAsnGlnIntyrglyGlyAspPhe 61
:
Qy 187 GAGACATTTGCTAGTGTGATGATACAATVGTGCAGTTAGTCAGGTACTATTGATCCGGT 246
||| ||| ||| : : : : : ||| ||| : : : : :
Db 62 GluThrPheIleAspSer-----GlyGluLeuSerAlatythrIleValVaIgly 78
:
Qy 247 ACTCTGTTAGCGGTATAGTGGGCTCACTTCTATATCCGACCGATAGGAATAATAGGT 306
||| ||| ||| ||| : : : : : ||| ||| : : : : :
Db 79 ThrValIleThrGlyPheGlyPheThrThr-----ProLeuGlyLeu----- 92
:
Qy 307 GCTATAATAATATCTTTTGGTACCCTAATCACTGTCTTTTGGCCGGGAGAACACAGAC 366
||| ||| ||| ||| : : : : : ||| ||| : : : : :
Db 93 --AlaLeuIleGlyPheGlyThrLeuIleProValLeuPheProAlaGlnAspGlnSer 111
:
Qy 367 AAAACAGTATGGACACAATTTATTAAATGGGAGAAATTTTGTGTGATCACCGCTTAACA 426
||| ||| : : : : : ||| ||| : : : : :
Db 112 AsnThr---TrpSerAspPheIleThrGlnThrLysAsnIleIleLysGluIleAla 130
:
Qy 427 GAAGCATAAAAACAGCTAAAGCTTACAACCTTTAGAAGGATTTACACAAAATATTACAAAGC 486
: : : : : ||| ||| : : : : : ||| ||| : : : : :
Db 131 SerThrTyrlleSerAsnAlaAsnLysIleLeuAsnArgSerPheAsnValIleSerThr 150
:
Qy 487 TATAATACAGCATTAGATGATGGAGAAAATTTAAAAAGACTACAAAGCTCTCGGATTACCA 546
||| ||| ||| ||| : : : : : ||| ||| : : : : :
Db 151 TyrHisAsnHisLeuLysThrTIpGlu-----AsnAsnProAsnProGln 165
:
Qy 547 CCATCATCGCATTTACAAAGCTGCCCTGTGACTCTTAAATACGATTTGAGAATGTCAC 606
: : : : : ||| ||| : : : : : ||| ||| : : : : :
Db 166 AsnThrGlnAspValArgThrGlnIleGlnLeuValHisTyrlHisPheGlnAsnValile 185
:
Qy 607 AATGATTTTATTCGAGAAATACCT-----GGTTTCCAACCTTGAAACTTATAAAACGCTA 660
: : : : : ||| ||| : : : : : ||| ||| : : : : :
Db 186 ProGlnLeuValAsnSerCysProProAsnProSerAspCysAspTyrltyrAsnIleLeu 205
:
Qy 661 TTACTACCTATTATTGCGCAAGCTGCTAAATTTTCATTTAAATTTATTACAAAGAGTGCT 720
: : : : : ||| ||| : : : : : ||| ||| : : : : :
Db 206 ValLeuSerSertyrAlaGlnAlaAlaAsnLeuHisLeuThrValLeuAsnGlnAlaVal 225
:
Qy 721 GAATVGGCTGAATGGAATGCGAGATATACATCCTTCACAAATTAACCTAATGCTGGGA 780
: : : : : ||| ||| : : : : : ||| ||| : : : : :
Db 226 LysPheGluAlatyrlLeuLysAsnAsnArgGlnPheAspTyrlLeuGluPro---LeuPro 244
:
Qy 781 ACATCAGATGACTATTATAACITTTTAAAGAAAATATACCTAAATATAGTACTAATTTGT 840
||| ||| ||| ||| : : : : : ||| ||| : : : : :
Db 245 ThrAlaIleAspTyrltyrProValLeuThrLysAlaIleGluAspTyrlThrAsnTyrcys 264
:
Qy 841 GCAAATACCTATAGAGAGGACTAAATAAACTTCGAAACGAACT----- 885
||| ||| ||| ||| ||| : : : : : ||| ||| : : : : :
Db 265 ValThrThrTyrllysLysGlyLeuAsnLeuIleLysThrProAspSerAsnLeuAsp 284
:
Qy 886 ---AATATGAGATGGAGPATTAATTAATGATTATCGAAGATATATGACTATPACTGTATTA 942
||| ||| ||| ||| : : : : : ||| ||| : : : : :
Db 285 GlyAsnIleAsnTpAsnThrTyrcAsnThrTyrcArgThrLysMetThrThrAlaValLeu 304
:
Qy 943 GATACTATCGTCAATTTCTTTTTTATCATATAAAGAGATACAAAGATTCAATAGGAGA 1002
||| ||| ||| ||| : : : : : ||| ||| : : : : :
Db 305 AspLeuValAlaLeuPheProAsnTyrltyrAspValGlyLysTyrlProIle----- 320
:
1003 ATAGTGGCATTAACCTGAACCTTACAGAGAAATTTATACAACTGAAATAAAATTTTGAC 1062

[illegible]

Db	300	IleGluLeuTyrThrGluSerValaleGluGlyAspTyrLeuSerGlyIle-	316
Qy	1216	AATAGATCTACTTATGCTTACACAGGAACCTAAATTT	1260
Db	317	---ArgGluSerLysTyrThrGlyAsnGlnPhePheThrMetLysAsnIleTyrGly	335
Qy	1261	GAAGAACAAGGTCCACCCACACAAAA-	1302
Db	336	Asn-----ThrAsnArgLeuSerLysGlnLeuIleThrLeuLeuProGly	350
Qy	1303	GAATCCCTATAAAGTTCAATTTGTAACTGATAGACAGTAACCTCTACTTCCCTTTTCT	1362
Db	351	Glu---PheMetThrHisLeuSerIleAsnArgProPheGlnThrIleAlaGlyIleAsn	369
Qy	1363	AACATATCTTTACAAATAATTAACAAATGMACTTTATTAAATAATTCACCTAGTAAATAA	1422
Db	370	LysLeuTyrSerLeuIleGlnLysIle-----ValPheThrThrPheLysAsnAsp	386
Qy	1423	TTAAATATATTACAGTCGGGGGAATTTATCTAATGAT-----AAAAAAACAACCTGAT	1473
Db	387	AsnGluTyrGlnLysAsnPheAsnValAsnAsnGlnAsnGluProGlnGluThrThrAsn	406
Qy	1474	TTTCAATTTCTGTAAAAAAGACTGTAACCAATATTATCAATTCACAAATTTGTTTACCAAGC	1533
Db	407	Tyr-----ProAsnAspTyrGlyGly	413
Qy	1534	TATATAGT-----TATAGTCATATTTTATCCAGTTTCTTCTTTATTTAATTTCTCTAT	1587
Db	414	SerAsnSerGlnLysPheLysHisAsnLeuSerHisPheProLeuIleIleHisLysLeu	433
Qy	1588	AAATTTGGATTAGCGCTAAATATATATATATATATACAGTGCATTTAGGATGGACACACAGTAGT	1647
Db	434	GluPheAlaGluTyrPheHisSerIlePhe-----AlaLeuGlyTyrThrHisAsnSer	451
Qy	1648	GTTAATAGAAATATGCAATATACAGATAAATAATTAACATGATGCCAGCATCAAGAGT	1707
Db	452	ValAsnSerGlnAsnLeuIleSerGluSerValSerThrGlnIleProLeuValLysAla	471
Qy	1708	AACAGTCTTGATACAAACTCTAAAGTAAATGAAGGACTGTGTATACAGAGGAAACTTG	1767
Db	472	TyrGluVal---ThrAsnAsnSerValIleargGlyProGlyPheThrGlyAspLeu	490
Qy	1768	GTTTATTTACAAAGTCAAGGCGTTTAGAGATATACATGTAGAACTCCTAATTTCTACACAA	1827
Db	491	IleGluLeuArgAsp-----LysCysSerIleLysCysLysAla---SerSerLeuLys	507
Qy	1828	TCATTATACATAGACTTCGATACGCTACAAATGGTGTCTGGAATATCTCTTCCTAATATA	1887
Db	508	LysTyrAlaIleSerLeuPheTyrAlaAlaAsnAsnAlaIleAlaValSerIleAspVal	527
Qy	1888	TCTCTTACAATACCAGGAGTAATAAGGAATACCACCTCAACGACTCAACACACTTTTCT	1947
Db	528	GlyAspSerGlyAlaGlyValLeu-----LeuGlnProThrPheSer	541
Qy	1948	GGTACAAATATATAATAT-----TTACAATACGAGAGATTTGGGTATTTCT	1992
Db	542	ArgLysGlyAsnAsnAsnPheThrIleGlnAspLeuAsnTyrLysAspPheGlnTyrHis	561
Qy	1993	CAATTTCCAAGTACAGTAACATTTACCTTTTAAATCGAAACATACCATTTATTTAATTCGT	2052
Db	562	ThrLeuLeuValAspIleGluLeuProGluSerGluGluIleHisIleHisLeuLysArg	581
Qy	2053	GCAGAT-----GTATCAAAATTCATTTTATCATTCATTAATTTGAATTTATACCAATT	2106
Db	582	GluAspAspTyrGluGluGlyValIleLeuLeuIleAspLysLeuGluPheLysProIle	601
Qy	2107	ACTTCTCTGTACGCCAAAATAGAGAAAAACAAAAATTAGAAACTATCCCAACAAAAATA	2166
Db	602	AspGluAsnTyr-----ThrAsnGluMetAsnLeuGluLysAlaLysLysAlaVal	618
Qy	2167	AATACATTTTTCACAAATCATACAAAAAATCTTTTAAATATAGAAAGCCACAAATATGAT	2226

Db	619	AsnValIleuPheIleAsnAlaThr---AsnAlaIeuLysMetAspValThrAspTyrHis	637
Qy	2227	ATTGAT 2232 	
Db	638	IleAsp 639	
RESULT 11			
ADF31302			
ID	ADF31302	standard; protein; 1109 AA.	
XX	AC	ADF311302;	
XX	DT	12-FEB-2004 (first entry)	
XX	DE	Bacillus thuringiensis serovar finitimus cry28Aa1 delta-endotoxin.	
XX	KW	Cry26Aa1; cry28Aa1; delta-endotoxin; insect pest control;	
XX	KW	transgenic plant; insect resistance; insecticide.	
XX	OS	Bacillus thuringiensis serovar finitimus.	
XX	FN	US2003150018-A1.	
XX	PD	07-AUG-2003.	
XX	PF	15-JAN-2003; 2003US-00345020.	
XX	PR	08-JAN-2000; 2000US-0175158P.	
XX	PR	08-JAN-2001; 2001US-00756526.	
XX	PA	(WOJC/) WOJCIECHOWSKA J A.	
XX	PA	(LEWI/) LEWITIN B I.	
XX	PA	(ZALU/) ZALUNIN I A.	
XX	PA	(REVI/) REVINA L P.	
XX	PA	(CHES/) CHESTUKHINA G G.	
XX	FI	Wojciechowska JA, Lewitin EI, Zalunin IA, Revina LP;	
XX	FI	Chestukhina GG;	
XX	DR	WPI; 2003-897623/82.	
XX	DR	N-PSDB; ADF31301.	
XX	FT	New isolated nucleic acid molecule encoding a toxin that is active	
XX	FT	against insects useful for controlling insect pests or for conferring	
XX	FT	insect resistance in plants.	
XX	PS	Claim 22; SEQ ID NO 4; 42pp; English.	
XX	CC	The present invention relates to the isolation of novel cry26Aa1 and	
XX	CC	cry28Aa1 delta-endotoxin genes from <i>Bacillus thuringiensis</i> ssp.	
XX	CC	finitimus. The sequences for the delta-endotoxin polypeptides are also	
XX	CC	disclosed. The invention provides methods for producing the toxins and	
XX	CC	compositions containing the toxins. The methods and sequences of the	
XX	CC	invention are useful for controlling insect pests in transgenic plants to	
XX	CC	confer insect resistance. The present sequence represents the cry28Aa1	
XX	CC	delta-endotoxin of the invention.	
XX	SQ	Sequence 1109 AA;	

Alignment Scores:	
Pred. No.:	6.49e-67
Score:	901.00
Percent Similarity:	49.29%
Best Local Similarity:	34.19%
Query Match:	22.87%
DB:	7
Gaps:	27
Indels:	114
Mismatches:	242
Conservative:	106
Matches:	240
Length:	1109

US-10-782-570-1 (1-2235) x ADF31302 (1-1109)

Qy 199 AGTCTGATCAAAVTGCTGCAGTTAGTCAGGTACTATTGTATCCGTACTCTGTTAGCC 258

Db 28 SerSerAspThrValAlaValSerAlaGlyIleValValGlyThrIleLeuThr 47

Qy	259	GGTATAGGTGGCGCTCACTTCTATATCCGGACCGAGTAAGTAATAATAGGTGCTCTAATAATA 318
Db	48	-----AlaPheAlaSerPheValaAsnPro-----GlyValValLeuLeu 60
Qy	319	TCCTTTGGTACCCCTAATCACTGTCTTTTGGCCGCGGAGAACAAAGAC---AAAAACAGTA 375
Db	61	SerPheGlyThrLeuAlaProValLeuTrpAspProGluGluAspProLysLeuLeu 80
Qy	376	TGGACACAAATTTATTAATAATGGGAGAAATTTTGTGTGATACACCGTTAAACAGAAAGCAT 435
Db	81	TrpSerGlnPheMetLysHisGlyGluAspLeuLeuAsnGlnThrIleSerThrAlaVal 100
Qy	436	AAACAGCTAAAGTTACAACTTTAGAGAGATTTAGACAAATATATACAAAGCTATAATACA 495
Db	101	LysGluIleAlaLeuAlaHisLeuAsnGlyPheLysAspValLeuThrTyrtyrGluArg 120
Qy	496	GCATTACATGATGGAGAAATTAATAAGACTACAAGCTCTCGATTACCAACCATCATCA 555
Db	121	AlaPheAsnAspTrpLysArg-----AsnProSerAla 131
Qy	556	GCATTACAAACAGCTGCCTTGACTCTTAAATAATACGATTTGAGAAATGTTCAATGATTTT 615
Db	132	-----AsnThrAlaArgLeuValSerGlnArgPheGluAsnAlaHisPheAsnPhe 148
Qy	616	ATTCGAGAAATACCTGGTTTCCAACTTTGAAACTATAAAAGCTATTACTACTATTTAT 675
Db	149	ValSerAsnMetProGlnLeuGlnLeuProThrTyrtyrAspThrLeuLeuLeuSerCysTyr 168
Qy	676	GCGCAAGCTCTAATTTTCAATTAATTAATTAACAACAGGTCTGNAATGGCTGATGAA 735
Db	169	ThrGluAlaAlaAsnLeuHisLeuAsnLeuLeuHisGlnGlyValGlnPheAlaAspGln 188
Qy	736	TGGAATGCAGATATACATCTCTCAAAATTCGAACCTTAATCTCGTGAACATCAGATGACT 795
Db	189	TrpAsnAlaAspGlnProHisSerProMetLeuLysSerSerglyThr-----Tyr 205
Qy	796	TATAAATCTTTTAAAGAAATATACCTAAATATAGTAACCTATTGTGCAAAATACCTATAGA 855
Db	206	TyrAspGluLeuLeuValTyrIleGluLysTyrIleAsnTyrCysThrLysThrTyrHis 225
Qy	856	GAAGGACTAATAAATTCGAAACGAACCTAATATGAGATGGAGTATATTATGATTAT 915
Db	226	LysGlyLeuAsnHisLeuLysGluSerGluLysIleThrTrpAspAlaTyrAsnThrTyr 245
Qy	916	CGAAGATATGACTATTACTGTATTAGATACTATCGTCAATTTCTTTTATGATATA 975
Db	246	ArgArgGluMetThrLeuIleValLeuAspLeuValAlaThrPheProPheTyrAspIle 265
Qy	976	AAGHAGATACAAAGATTCATAGGAGAATAGGTGGCAATTAAACTGAACCTTACAAGAGAA 1035
Db	266	ArgArgPhePro-----ArgGlyValGluLeuGluLeuThrArgGlu 279
Qy	1036	ATTATACAACTGAATAAATTTTGACCGTCTTACTTACCTGGAATTCACCAATCTC 1095
Db	280	ValTyrThrSer-----LeuAspHisLeuThrArgProProGly--- 292
Qy	1096	GCTATAATGGAATATATATTTAAACAGTTTCAGGCGTTAGATTATTTTCATTTTAGATGAA 1155
Db	293	-----LeuPheThrTrpLeuSerAsp 299
Qy	1156	CTTATATTTTATACAAAAAATGAAACGTACGGGAATCGTTTAGTTGGTATTTGGGAATCGT 1215
Db	300	IleGluLeuTyrThrGluSerValAlaGluGlyAspTyrLeuSerGlyIle----- 316
Qy	1216	AATAGATCTATTATGCTACGACAGGAACCTGAATTT-----ATATATGGA 1260
Db	317	---ArgGluSerLysTyrTyrThrGlyAsnGlnPhePheThrMetLysAsnIleTyrGly 335
Qy	1261	GAAAGAACAGGTCCACCCACAACAAA-----ACCTTAATACCAATTT 1302
Db	336	Asn-----ThrAsnArgLeuSerLysGlnLeuIleThrLeuLeuProGly 350
Qy	1303	GAATCTCTAATAAGTTTCAATTTGTAACGTAGACAGTAAGTAAGTCTCTACTCTCCCTTTTCCT 1362

		:::	:::	:::	:::	
Db	351	Glu----	PheMetThrHisLeuSerIleAsnArgProPheGlnThrIleAlaGlyIleAsn	369		
QY	1363	AACATACATCTTTACAATAATCAAAATTGAACCTTTTAAATAAATTAATCCACCTAGTAGATAAA	1422			
Db	370	LysLeuTyrrSerLeulleGlnLysIle-	-----ValPheThrThrPheLysAsnAsp	386		
QY	1423	TTCACATATTACGTGGGGGGAATTTATCTTCAATGAT-----AAAAAACAACTGAT	1473			
Db	387	AsnGluTyrrGlnLysAsnPheAsnValAsnAsnGlnAsnGluProGlnGluThrThrAsn	406			
QY	1474	TTTTCAAATTCCTGTAAAAAAGACTGTAAACCAATATTAAATCCAATGTTTACCAGGC	1533			
Db	407	Tyr-----	-----ProAsnAspTyrrGlyGly	413		
QY	1534	TATATAAGT-----TATATGTCATATTTTATCCAGTTTTTCTTATTATTAATATTCTCAT	1587			
Db	414	SerAsnSerGlnLysPheLysHisAsnLeuSerHisPheProleulleIleHisLysLeu	433			
QY	1588	AAAATTCGATTAGCGCTPAATATATTATATAPACAGGTGCATTTAGATGGACACACAGTAGT	1647			
Db	434	GluPheAlaGluTyrrPheHisSerIlePhe-----AlaLeuGlyTrpThrHisAsnSer	451			
QY	1648	GTTHATAGAATAATGCAATATCAGATAAATAATTTACAATGATCCCAGCAATCAAAAGT	1707			
Db	452	ValAsnSerGlnAsnLeulleSerGluSerValSerThreGlnIleProleuValLysAla	471			
QY	1708	AACAGTCTTGATACAAACTCTTAAGGTAAATTTGAAGGACCTGGTCATACAGAGCAAACTTG	1767			
Db	472	TyrrGluVal---ThrAsnAsnSerValIleargGlyProGlyPheThrGlyLysAspLeu	490			
QY	1768	GTTPATTTACAAAGTCAAGCGCTTTAGAGATTACATGTAGAACTCCTAATTCTCACAA	1827			
Db	491	IleGluLeuArgAsp-----LysCysSerIleLysCysLysAla---SerSerLeuLys	507			
QY	1828	TCITTATTACATTAGACTTCGATACGCTACAAATGGTGTGCGAAATACTCTTCCTAATATA	1887			
Db	508	LysTyrrAlaIleSerLeuPheTyrrAlaAlaAsnAsnAlaIleAlaValSerIleAspVal	527			
QY	1888	TCTCTTACAATACCAGGAGTAATAGGAATACCACCTCAACGAGCTCAACACACTTTTTCT	1947			
Db	528	GlyAspSerGlyAlaGlyValLeu-----LeuGlnProThrPheSer	541			
QY	1948	GGTACAAATATATAATAT-----TTACAATACGAGATTTTGGGTATTTTC	1992			
Db	542	ArgLysGlyAsnAsnAsnPheThrIleGlnAspLeuAsnTyrrLysAspPheGlnTyrrHis	561			
QY	1993	CAATTTCCAAGTACAGTAACATTACTCTTTAAATCGAAACATACCATTTATTTAATCGT	2052			
Db	562	ThrLeuLeuValAspIleGluLeuLeuProGluSerGluGluIleHisIleHisLeuLysArg	581			
QY	2053	GCAGAT-----GPATCAAAATCAATTTTAAATCATGATAAAATTTGAATTTATACCAATT	2106			
Db	582	GluAspAspTyrrGluGluGlyValIleLeuLeulleaspLysLeuGluPheLysProIle	601			
QY	2107	ACTTCTCTGTGACGCCAAAATAGAGAAAAAATAATTAGAAATCTACCAACAAATAAATA	2166			
Db	602	AspGluAsnTyrr-----ThrAsnGluMetAsnLeuGluLysAlaLysAlaVal	618			
QY	2167	AATACATTTTTCACAAATCATACAAAANAATCTTTTAAATATAGAGCCACAACTATGAT	2226			
Db	619	AsnValLeuPheIleAsnAlaThr---AsnAlaLeuLysMetAspValThrAspTyrrHis	637			
QY	2227	ATTGAT	2232			
Db	638	IleAsp	639			
RESULT 12						
ID	ADF31307					
XX	ADPF31307 standard; protein; 1109 AA.					
XX	ADPF31307;					
AC						

DT 12-FEB-2004 (first entry)
 XX *Bacillus thuringiensis* serovar finitimus cry28Aa1 delta-endotoxin.
 DE *Cry26Aa1*; *cry28Aa1*; delta-endotoxin; insect pest control;
 XX transgenic plant; insect resistance; insecticide.
 KW *Bacillus thuringiensis* serovar finitimus.
 XX
 OS US2003154510-A1.
 XX
 PN 14-AUG-2003.
 XX
 PD 15-JAN-2003; 2003US-00342821.
 XX
 PP 07-JAN-2000; 2000US-0175158P.
 PR 08-JAN-2001; 2001US-00756526.
 XX
 PP (WOJC/) WOJCIECHOWSKA J A.
 PA (LEWI/) LEWITIN E I.
 PA (ZALU/) ZALUNIN I A.
 PA (REVI/) REVINA L P.
 PA (CHES/) CHESTUKHINA G G.
 XX
 XX Wojciechowaka JA, Lewitin EI, Zalunin IA, Revina LP;
 PI Chestukhina GG;
 PI
 XX
 DR WPI; 2003-897757/82.
 DR N-PSDB; ADF31306.
 XX
 XX New delta-endotoxin nucleic acid molecules, *cry26Aa1* and *cry28Aa1*, useful
 PT for controlling insect pests and for conferring insect resistance.
 XX
 XX Claim 22; SEQ ID NO 4; 42pp; English.
 PS
 XX The present invention relates to the isolation of novel *cry26Aa1* and
 CC *cry28Aa1* delta-endotoxin genes from *Bacillus thuringiensis* spp.
 CC finitimus. The sequences for the delta-endotoxin polypeptides are also
 CC disclosed. The invention provides methods for producing the toxins and
 CC compositions containing the toxins. The methods and sequences of the
 CC invention are useful for controlling insect pests in transgenic plants to
 CC confer insect resistance. The present sequence represents the *cry28Aa1*
 CC delta-endotoxin of the invention.
 XX
 SQ Sequence 1109 AA;

Alignment Scores:
 Pred. No.: 6,49e-67 Length: 1109
 Score: 901.00 Matches: 240
 Percent Similarity: 49.29% Conservative: 106
 Best Local Similarity: 34.19% Mismatches: 242
 Query Match: 22.87% Indels: 114
 DB: 7 Gaps: 27

US-10-782-570-1 (1-2235) x ADF31307 (1-1109)

QY 199 AGTGTGATACAAATGTCGAGTAGTCAGGACTATTGTATCGGTACTCTGTAGCC 258
 DB 28 SerSerAspThrValAlaValValSerAlaGlyIleValValGlyIleLeuThr 47
 QY 259 GGTATAGGTGGCTCACCTCTATATCCGACCGATAGGAATAATAGTGTATATA 318
 DB 48 -----AlaPheAlaSerPheValAsnPro-----GlyValValLeuIle 60
 QY 319 TCTTTTGTGACCTAATCACTGTCTTTTGGCCCGGGGAGAACAGAC-AAAACAGTA 375
 DB 61 SerPheGlyThrLeuAlaProValLeuTrpProAspProGluGluAspProLysIle 80
 QY 376 TGGACACAAATTTAATAATGGGAAATTTTGTGTATACACCGTTAAACAGAAAGCAT 435
 DB 81 TrpSerGlnPheMetLysHieGlyGluAspLeuLeuAsnGlnThrIleSerThrAlaVal 100
 QY 436 AAACAGCTAAAGTTACAAAC-TTAGNAGGATTTAGACAAATATTACAAAGCTATAATACA 495

DB 101 LysGluIleAlaLeuAlaHisLeuAsnGlyPheLysAspValLeuThrTrpTyGluArg 120
 QY 496 GCATTAGATGATGGAGAAAATTAAGAAAGACTACAAGCTCCTGGATTACCAACCATCATCA 555
 DB 121 AlaPheAsnAspTrpLysArg-----AsnProSerAla 131
 QY 556 GCATTACACAAAGCTGCTTGACTCTTTAAATACGATTTGAGAATGTTCAACATGATTTT 615
 DB 132 -----AsnThrAlaArgLeuValSerGlnArgPheGluAsnAlaHisPheAsnPhe 148
 QY 616 ATTCGAGAAAATACCTGCTTCCAACTTGAACCTTATAAAGCTATTACTACTATTATTAT 675
 DB 149 ValSerAsnMetProGlnLeuGlnLeuProThrTrpAspThrLeuLeuLeuSerCysTyr 168
 QY 676 GCGCAAGCTGCTAATTTTCAATTTAATTAACAACAGGTGCTGTAATTTGGCTGATGAA 735
 DB 169 ThrGluAlaAlaAsnLeuHisLeuAsnLeuHisGlnGlyValGlnPheAlaAspGln 188
 QY 736 TGGATCGCATATATACCTCTTCAAAATTTGAACCTAATGCTGGAACATCAGATGACTAT 795
 DB 189 TrpAsnAlaAspGlnProHisSerProMetLeuLysSerSerGlyThr-----Tyr 205
 QY 796 TATAAACTTTTAAAGAAAATATATACCTAAATATAGTAACCTATTCTGCAAAATACCTATAGA 855
 DB 206 TyrAspGluLeuLeuValTyrIleGluLysTyrIleAsnTyrCysThrLysThrTyrHis 225
 QY 856 GAAGGACTAAATAAATTCGAAACGAACTAATATAGATGGAGTATATTAATGATATAT 915
 DB 226 LysGlyLeuAsnHisLeuLysGluSerGluLysIleThrTrpAspAlaTyrAsnThrTyr 245
 QY 916 CGAAGATATATGACTATTACTGTATATAGACTACTACCTCAATTTCTTTTATGATATA 975
 DB 246 ArgArgGluMetThrLeuIleValLeuAspLeuValAlaThrPheProPheTyrAspIle 265
 QY 976 AAGAGATACAAAGATTCAATAGGAAGAATAGGTGGCAATTAACCTGAACTTACAAAGAA 1035
 DB 266 ArgArgPhePro-----ArgGlyValGluLeuGluLeuThrArgGlu 279
 QY 1036 ATTATACAACCTGAATAAATTTTGACCGTCTTACTTACCTTGAATTTCAACCAACTCTC 1095
 DB 280 ValTyrThrSer-----LeuAspHisLeuThrArgProGly--- 292
 QY 1096 GCTATAATGGAATATATTAACACGTTACGGCTTAGATATTTTCTATTATAGTAA 1155
 DB 293 -----LeuPheThrTrpLeuSerAsp 299
 QY 1156 CTTATATTTTATACAAAATGAAACGTCACGGAAATCGTTAGTTGGTATTTCGAAATCGT 1215
 DB 300 IleGluLeuTyrThrGluSerValAlaGluGlyAspTyrLeuSerGlyIle----- 316
 QY 1216 AATAGATCTACTTATGCTACGACGAGAACTGAAAT-----ATATATGGA 1260
 DB 317 ---ArgGluSerLysTyrTyrThrGlyAsnGlnPhePheThrMetLysAsnIleTyrGly 335
 QY 1261 GAAGAACACGCTCCACCACCAACAAA-----ACTTTAATACCATTT 1302
 DB 336 Asn-----ThrAsnArgLeuSerLysGlnLeuIleThrLeuLeuProGly 350
 QY 1303 GAATCCTATAAGTTTCAATTTGTAACCTAGATACAAAGTAACCTACTCTCCCTTTTCTCT 1362
 DB 351 Glu---PheMetThrHisLeuSerIleAsnArgProPheGlnThrIleAlaGlyIleAsn 369
 QY 1363 AACATATACCTTTCAATTAATCAAAATGAACTTTTATTTAATAATCACTCCTAGTAATAA 1422
 DB 370 LysLeuTyrSerLeuIleGlnLysIle-----ValPheThrThrPheLysAsnAsp 386
 QY 1423 TTAACATATTCAGCTGGGGGAATTTATCTAATGAT-----AAAAAACAACCTGAT 1473
 DB 387 AsnGluTyrGlnLysAsnPheAsnValAsnAsnGlnAsnGluProGlnGlnThrAsn 406
 QY 1474 TTTCAATTTCTGTGTAAGAAAGACTGTAAACCAATATTATTAATCCAAATTTGTTACCAAGC 1533
 DB 1533

407	Tyr	-----ProAsnAspTyrGlyGly	413
1534	TATAATAGT	-----TATAGTCATATTTTATCCAGGTTTCTTATTAAATTAATTCCTAT	1587
414	SerAsnSerGlnLysPheLysHisAsnLeuSerHisPheProLeuIleIleHisLysLeu	433	
1588	AAAAATTGGATTAGCGCTAAATATATTATATACACAGGTGCATTAGGATGGACACACAGTAGT	1647	
434	GlupheAlaGluTyrPheHisSerIlePhe	-----AlaLeuGlyTyrThrHisAsnSer	451
1648	GTTAATAGAAATATATGCATATCATGATATAAATAATTAACAATGATCCAGCAATCAAGAAGT	1707	
452	ValAsnSerGlnAsnLeuIleSerGluSerValSerThrGlnIleProLeuValLysAla	471	
1708	AACAGCTCTTGATACAAACTCTAGGTTAATTGAAGGACCTGGTCATACAGGAGGAAACTTG	1767	
472	TyrGluVal	---ThrAsnAsnSerValIleArgGlyProGlyPheThrGlyGlyAspLeu	490
1768	GTTTATTATACAAAGTCAAGCGGCTTTAGAGATTATCATGTAGAACTCCTTAATTTCTACACAA	1827	
491	IleGluLeuArgAsp	-----LysCysSerIleLysCysLysAla---SerSerLeuLys	507
1828	TCATTATACATTAGACTTCGATACGCTACAAATGGTGTCTGAAATACCTCTTCCTAATATA	1887	
508	LysTyrAlaIleSerLeuPheTyrAlaAlaAsnAsnAlaIleAlaValSerIleAspVal	527	
1888	TCTCTTACAATACCGAGGAGTAATAGGAATACCACTCAACGACTCAACACACTTTTCT	1947	
528	GlyAspSerGlyAlaGlyValLeu	-----LeuGlnProThrPheSer	541
1948	GGTACAAATATTATAAT	-----TTACAATACGAGAGATTTGGGTATTC	1992
542	ArgLysGlyAsnAsnAsnPheThrIleGlnAspLeuAsnTyrLysAspPheGlnTyrHis	561	
1993	CAATTTCCAGTACAGTAAACATTACCTTTAAATCGAAACATACCATTTATTTATTCGT	2052	
562	ThrLeuLeuValAspIleGluLeuProGluSerGluGluIleHisLysLeuLysArg	581	
2053	GCAGT	-----GTATCAAAATTCATTTTAAATCATGATAAAATTGAATTTATACCAATT	2106
582	GluAspAspTyrGluGluGlyValIleLeuLeuIleAspLysLeuGluPheLysProIle	601	
2107	ACTTCTCTGTACGCCAAAATAGAGAAAAAATAAATAATTAGAAACTATCCAAACAAAATA	2166	
602	AspGluAsnTyr	-----ThrAsnGluMetAsnLeuGluLysAlaLysLysAlaVal	618
2167	AATCATTTTTCACAAATCATACAAAAATATCTTTAAATATAGAAGCCACAACTATGAT	2226	
619	AsnValLeuPheIleAsnAlaThr	---AsnAlaLeuLysMetAspValThrAspTyrHis	637
2227	ATTGAT	2232	
638	IleAsp	639	

RESULT 13

ID	Accession	Protein	Length
AA063079	AA063079	standard; protein; 686 AA.	686
XX	AA063079		
AC	AA063079		
XX	AA063079		
DT	25-MAR-2003 (revised)		
DT	12-AUG-1995 (first entry)		
XX	XX		
XX	XX		
XX	XX		
DE	B.t. toxin PS71W3.		
XX	XX		
KW	Delta-endotoxin; crystal protein; biological control agent; Calliphorid;		
KW	screw-worm; sheep blowfly; Lucilia; Phormia; Calliphora; insecticide;		
KW	pesticide; B.t.		
XX	XX		
OS	Bacillus thuringiensis.		
XX	XX		
XX	XX		
PN	W09502694-A2.		
XX	XX		

Qy	544	CCACCATCATCGCATTAACAACAGCTGCCTTGACTCTTAAATAATACGATTTGAGAATGTT	603
Db	164	-----ThrHisAlaAsnAlaLysAlaValHisAspLeuPheThrThrLeuGluProIle	181
Qy	604	CACAAAT-----GATTTTATTCGAGAAATACCTGGTTTCCNACTTGGAACCTTATAAA	654
Db	182	IleAspLysAspLeuAspMetLeuLysAsnAsnAlaSerTyrArgIleProThr-----	199
Qy	655	ACGCTATTACTTACTATTATTCGCCAGCTGCTAAATTTTCATTTTAAATTTATTACACAA	714
Db	200	-----LeuProAlaTyrAlaGlnIleAlaThrTrpHisLeuAsnLeuLeuLysHis	216
Qy	715	GGTCTGGAATGGCTGATGAATGAATGCAGATATATCATCTTCACAAATGGAACCTTAAT	774
Db	217	AlaAlaThrTyrTyrAsnIleTrp-----LeuGlnAsnGlnGlyIleAsnProSer	233
Qy	775	GCTGGACATCAGATGACTATTATAA---CTTTTAAAGAAATATATACCTTAATATAGT	831
Db	234	ThrPheAsnSerSerAsnTyrTyrGlnGlyTyrLeuLysArgLysIleGlnGluTyrThr	253
Qy	832	AACATTATGTGCAATACCTATAGAGAAGGACTAAATAAATTCCTGAAACGAACTTAATATG	891
Db	254	AspTyrCysIleGlnThrTyrAsnAlaGlyLeuThrMetIleArgThrAsnThrAsnAla	273
Qy	892	AGATGGAGTATATTAAATGATTATCGAAGATATATGACTATTACTGTTAGATACTATC	951
Db	274	ThrTrpAsnMetTyrAsnThrTyrArgLeuGluMetThrLeuThrValLeuAspLeuIle	293
Qy	952	GCTCAATTTCTTTTATGATATATAAGAGATACAAAGATTCAATAGAGAATAGGTGGC	1011
Db	294	AlaIlePheProAsnTyrAspProGluLysTyrProIle-----Gly	307
Qy	1012	ATTAATAACTGAACCTTACAAGAGAATTTATACAACTGAAATAAATTTTGACCGCTTACT	1071
Db	308	ValLysSerGluLeuThrThrArgLysValTyr---ThrAsnValAsnSerAspThrPheArg	326
Qy	1072	TACTTGAAATTCACACCAATCTCGCTATATTAATGGAAATATAATTTAAACAGCTTCAGG	1131
Db	327	-----ThrIleThrGluLeuGluAsnGlyLeuThrArgAsnPro---	339
Qy	1132	AGATTATTTTCATTTTATAGAACTTATATTATTTATACAAATAAT-----	1176
Db	340	ThrLeuPheThrTrpIleAsnGlnGlyArgPheTyrThrArgAsnSerArgAspIleLeu	359
Qy	1177	GAACGGTAC-----GGGAATCGTTTACTTGCTATGCTATGCGAATCGTAAT	1218
Db	360	AspProTyrAspIlePheSerPheThrGlyAsnGlnMetAla-----	373
Qy	1219	AGATCTACTTATGCTACGACAGGAACCGAAATATATATATGAGAAAGAACAGGT---	1272
Db	374	--PheThrHisThrAsnAspAspArgAsnIleIleTrpGlyAlaValHisGlyHisIle	392
Qy	1273	---CCACCCACCAAAACCTTTAATACCAATTGAATCCCTAT-----AAGTT	1317
Db	393	IleSerGlnAspThrSerLysValPheProPheTyrArgAsnLysProIleAspLysVal	412
Qy	1318	TCAATTTGAATGATAGCAAGTAACCTCTACTTCCCTTTTCCCTAACATATATTTACA	1377
Db	413	GluIleValArgHisArgGlu-----TyrSerAsp	422
Qy	1378	ATTAATCAAAATGAACTTTATTTTAAATAATTCACCTAGTAAATAAATTAACATATTCAG	1437
Db	423	IleIleTyrGluMetIlePhePheSerAsnSer---SerGluValPheArgTyrSerSer	441
Qy	1438	GGGGGGAAATTTATCTAATGATATAAAAAACACTGATTTTCAAATTCCTGTAAAAAAAG	1497
Db	442	AsnSerThrIleGluAsnAsnTyrLysArgThrAspSerTyrMetIleProLysGlnThr	461
Qy	1498	TGTAACCAATTAATTAATCCAAATTTGTTTACCAAGCTATATATAGTTATATGCTATTTTA	1557
Db	462	TrpLys-----AsnLysGluTyrGlyHisThrLeu	471
Qy	1558	TCCAGTTTTCTTTTAAATTTATCTCATAAATTCGATTAGCGCTAAATATATATATAT	1617

D	b			SerTyrIleLysThrAspAsnTyrIlePheSerVal-----ValArgGluArgArg	488			
Q	y			ACAGGTGCATTAGATCGACACACAGTAGTGTTAATAAGAATAATCACTAATCATCAGATAAA	1677			
D	b			ArgValAlaPheSerTrpThrHisThrSerValAspPheGlnAsnThrIleAspLeuAsp	508			
Q	y			ATAATTACAATGATCCACGACAACTCAAAGGTAAACAGACTTCGATACAAACTCTAAGGGTAATT	1737			
D	b			AsnIleThrGlnIleHisAlaLeuLysAlaLeuLysValSerSerAspSerLysIleVal	528			
Q	y			GAAGGACTGGTCAATACAGGAGAACTTGGTTATTATTACAAAGTCAAGGCCGCTTAGAG	1797			
D	b			LysGlyProGlyHisThrGlyGlyAspLeuValIleLeuLysAspSer-----MetAsp	546			
Q	y			ATTACATGTAGA---ACTCCTAATCTCACACAATCTTATTACATTAGACTTCGATACGCT	1854			
D	b			PheArgValArgPheLeuLysAsnValSerArgGlnTyrGlnValArgIleArgTyrAla	566			
Q	y			ACAATGGTGTGGAATACTCTCTCTAATATATCTCTACAATACCAGAGTAATAGGA	1914			
D	b			ThrAsnAla-----ProLysThrValPheLeuThrGlyIleAspThr	581			
Q	y			ATACCACCTCAACGACTCAACAACACTTTTTCTGGTACAAAATTATAAT-----AATT	1968			
D	b			IleSerValGlu---LeuProSerThrThrSerArgGlnAsnProAsnAlaThrAspLeu	600			
Q	y			CAATACCGAGATTTGGGTATTTCCATTTCCCAAGTACAGTA-----	2010			
D	b			ThrTyrAlaAspPheGlyTyrValThrPheProArgThrValProAsnLysThrPheGlu	620			
Q	y			ACATTACCTTTAAATCGAAACATACCATTTATATTATTTAATCTGCAGATGTA	2061			
D	b			GlyGluAspThrLeuLeuMetThr-----LeuTyrGlyThrProAsnHis	635			
Q	y			TCAAAATCAATTTTAATCATGTATGAATAAATTGAAATTATACCAATTAATCTCTGTACGC	2121			
D	b			SerTyrAsnIle---TyrIleAspLysIleGluPheIleProIleThrGlnSerValLeu	654			
Q	y			CAAAATAGAGAAAAACAAAATTAGAACTATCCAAACAAAATAAATACATTTTTCACA	2181			
D	b			AspTyrThrGluLysGlnAsnIleGluLysThrGlnLysIleValAsnAspLeuPheVal	674			
Q	y			AATCAT	2187			
D	b			AsnAsn	676			
RESULT 14								
AAAR14374								
ID	AAAR14374	standard; protein; 675 AA.						
XX	AAAR14374;							
XX	27-AUG-2003	(revised)						
DT	25-MAR-2003	(revised)						
DT	04-FEB-1992	(first entry)						
XX	Dipteran active toxin.							
XX	Insecticide; B.t; crystal; delta endotoxin; cryIVC.							
OS	Bacillus thuringiensis serovar morrisoni.							
XX	EP457498-A.							
PD	21-NOV-1991.							
PF	09-MAY-1991;	91EP-00304180.						
XX	15-MAY-1990;	90US-00524255.						
PR	01-OCT-1990;	90US-00590903.						
XX	(MYCO) MYCOGEN CORP.							

XX Sick AJ;
 PI
 DR WPI: 1991-341902/47.
 DR N-PSDB; AAI4670.
 XX
 PT Bacillus thuringiensis genes encoding diptera-active toxins - and
 transformed microbials used to control insects in various environments.
 XX
 PS Claim 3; Page 15; 20pp; English.
 XX
 CC The sequence was deduced from the DNA sequence obtd. from plasmid
 CC pMYC1636 which was isolated from a genomic library prepd. from DNA from
 CC B.t. P871M3 [from B.t. P871M3-69 (NRRL B-1851)]. It is related to the
 CC cryIVC toxins from B.t. var. israelensis. The protein has a mol. wt. of
 CC 77 kD. Microorganisms transformed with the DNA may be administered to
 CC dipteran insects or their environ- ments, the expressed toxins acting as
 CC an insecticide. See also AARI4373. (Updated on 25-MAR-2003 to correct PA
 CC field.) (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 675 AA;

Alignment Scores:
 Pred. No.: 8,34e-67 Length: 675
 Score: 899.00 Matches: 251
 Percent Similarity: 47.96% Conservative: 114
 Best Local Similarity: 32.98% Mismatches: 268
 Query Match: 22.82% Indels: 128
 DB: 2 Gaps: 32

US-10-782-570-1 (1-2235) x AARI4374 (1-675)

QY 13 AATAATATGATATGATGATATCGATTCCAAAGATTTATCTATCTCTTAACAGAAAT 72
 DB 6 AsnLysAsnGluTyrGluLeuPheAsnAlaProSerAsnGlyPheSerLysSerAsn 25
 QY 73 ATTGATCATTTCTAGATACCTTACACAAATATCAAAATCAACCATTTACAAACACAAAT 132
 DB 26 -----TyrSerArgTyrProLeuAlaAsnLysProAsnGlnProLeuLysAsnThrAsn 43
 QY 133 TACAAGAGTGGCTCAATATGTCACAGGGAATACACATATGTCGATATTTTCGAGACA 192
 DB 44 TyrLysAspTrpLeuAsnValCysGlnAspAsnGlnTyrGlyAsnAsnAlaGlyAsn 63
 QY 193 TTTGCTAGTGTGATACATCTGCTGATGTCAGTCTGATGTCATGTCATGTCGCTGCTG 252
 DB 64 PheValSerSerGluThrLeuValGlyValSerAlaGlyIleValValGlyThrMet 83
 QY 253 TTAGCGGTATAGTGGGCTCACTTCTATATCCGACCGATAGGAAATATAGTGTCTATA 312
 DB 84 LeuGly-----AlaPheAlaAlaPro-----ValLeuAlaAlaGly 95
 QY 313 ATAATATCTTTGTTACCTATCTACTGCTTTTGGCCCGCGGAGAAACAGACAAACA 372
 DB 96 IleIleSerPheGlyThrLeuLeuProIlePheTrp---GlnGlySerAspProAlaAsn 114
 QY 373 GTATGACACAAATTTATTAATGCGAGAAATTTTGTGTATACACCGTTACAGAA--- 429
 DB 115 ValTrpGlnAspLeuLeuAsnIleGly-----GlyArgProIleGlnGluIle 130
 QY 430 -----AGCATAAACACGCTAAAGTTTACAAACTTTAGAGGATTTAGACAAATATACAA 483
 DB 131 AspLysAsnIleIleAsnValLeuThrSerIleValThrProIleLysAsnGlnLeuAsp 150
 QY 484 AGCTAATAACAGCATTAACACAGCTGCTGCTGCTTTAAATACGATTTGAGATGTT 603
 DB 164 -----ThrHisAlaAsnAlaValHisAspLeuPheThrThrLeuGluProIle 181
 QY 604 CACAAT-----GATTTTATTCGAGAAATACCTGGTTTCCAACTTCAAACTTATAAA 654

DB 182 IleAspLysAspLeuAspMetLeuLysAsnAsnAlaSerTyrArgIleProThr----- 199
 QY 655 ACGCTATTACTACCTATTATTCGCGCAAGCTCTAATTTTCAATTTTAAATTTATTACACAA 714
 DB 200 -----LeuProAlaTyrAlaGlnIleAlaThrTrpHisLeuAsnLeuLeuLysHis 216
 QY 715 GGTGCTGAATGGCTGATGAATGCAGATATACATCTCTTCAAAATTCGAACCTAAT 774
 DB 217 AlaAlaThrTyrTyrAsnIleTrp-----LeuGlnAsnGlnGlyIleAsnProSer 233
 QY 775 GCTGGAACATCAGATGACTATTATAA---CTTTTAAAGAAATATACCTAAATATAGT 831
 DB 234 ThrPheAsnSerSerAsnTyrTyrGlnGlyTyrLeuLysArgLysIleGlnGluTyrThr 253
 QY 832 AACTATTCTGCACAAATACCTATAGAGAGAGACTTAATAAATTCGAAACGAACTAATATG 891
 DB 254 AspTyrCysIleGlnThrTyrAsnAlaGlyLeuThrMetIleArgThrAsnThrAsnAla 273
 QY 892 AGATGGAGTATATTAATGATTCATTCGAAGATATATGACTATTACTGTATTAGATATATC 951
 DB 274 ThrTrpAsnMetTyrAsnThrTyrArgLeuGluMetThrLeuThrValLeuAspLeuIle 293
 QY 952 GCTCAATTTTCTTTTATGATATAAAGAGATACAAAGATTCATAGGAGAAATAGTGGC 1011
 DB 294 AlaIlePheProAsnTyrAspProGluLysTyrProIle-----Gly 307
 QY 1012 ATTAAACTGAACTTACAGAGAAATTTATACACTGAAATATAATTTTACCGCTTACT 1071
 DB 308 ValLysSerGluLeuThrArgGluValTyr---ThrAsnValAsnSerAspThrPheArg 326
 QY 1072 TACCTTGAAATTCACCCCAATCTCGCTATATGGAATATATTTAACACGTTTCAGGGCT 1131
 DB 327 -----ThrIleThrGluLeuGluAsnGlyLeuThrArgAsnPro--- 339
 QY 1132 AGATTATTTTCATTTTATAGTGAATATATTTTATACAAAAAT----- 1176
 DB 340 ThrLeuPheThrTrpIleAsnGlnGlyArgPheTyrThrArgAsnSerArgAspIleLeu 359
 QY 1177 GAAACGTAC-----CGGAATCGTTTGTAGTTGGTATCGGAATCGTAAT 1218
 DB 360 AspProTyrAspIlePheSerPheThrGlyAsnGlnMetala----- 373
 QY 1219 AGATCTACTTATGCTACGACAGAACTGAAATATATATATGAGAGAAAGACAGT----- 1272
 DB 374 ---PheThrHisThrAsnAspArgAsnIleIleTrpGlyAlaValHisGlyHisIle 392
 QY 1273 ---CCACCCACACAAAAAATTTAATACATTTGAATCTCTAT-----AAAGTT 1317
 DB 393 IleSerGlnAspThrSerLysValPheProPheTyrArgAsnLysProIleAspLysVal 412
 QY 1318 TCATTTGTAACGTAGTACAGTAATCTCTACTCTCCCTTTTCTCAACATATATTTACA 1377
 DB 413 GluIleValArgHisArgGlu-----TyrSerAsp 422
 QY 1378 ATTAATCAAAATGAACTTTTATTAATAATTCACCTAGTAATAATAATTAACATATCAGCT 1437
 DB 423 IleIleTyrGluMetIlePhePheSerAsnSer---SerGluValPheArgTyrSerSer 441
 QY 1438 GGGGGGAATTTATCTAATGATATAAAAAACAACTGATTTTCAATTTCTCTGTAATAAAGAC 1497
 DB 442 AsnSerThrIleGluAsnAsnTyrLysArgThrAspSerTyrMetIleProLysGlnThr 461
 QY 1498 TGTAACCAATTTATTAATCCAAATTTGTTTACCAGCTATATAGTATTAGTATATTTTAA 1557
 DB 462 TrpLys-----AsnLysGluTyrGlyHisThrLeu 471
 QY 1558 TCCAGTTTCTTTTATTAATTTATCTATAAATTTGGATTAGCGCTAAATATATATAT 1617
 DB 472 SerTyrIleLysThrAspAsnTyrIlePheSerVal-----ValArgGluArgArg 488
 QY 1618 ACAGGTGCATTAGGTAGGACACACAGTAGTGTGTTAATAGAAATATGCAATATACAGATAA 1677

Db 489 ArgValAlaPheSerTyrThrHisThrSerValAspPheGlnAsnThrIleAspLeuAsp 508
 QY 1678 ATAATTACATGATCCAGCAATCAAGGTAACTCTTGATACAACTCTTAAGTAATT 1737
 Db 509 AenIleThrGlnIleHisAlaLeuLysAlaLeuLysValSerSerAspSerLysIleVal 528
 QY 1738 GAAGGACCTGGTCATACAGGAGAACTTGGTTTATTACAAAGTCAAGGGGTTTAGAG 1797
 Db 529 LysGlyProGlyHisThrGlyLysAspLeuValIleLeuLysAspSer-----MetAsp 546
 QY 1798 ATTACATGTAGA---ACTCCTAATTCTACACAATCTTATTACATTAGACTTCGATACGCT 1854
 Db 547 PheArgValArgPheLeuLysAsnValSerArgGlnTyrGlnValArgIleArgTyrAla 566
 QY 1855 ACAATGGTGGTGGAAATCTCTCTTAATATATCTCTTACAAATACCAAGGAGTAATAGGA 1914
 Db 567 ThrAsnAla-----ProLysThrThrValPheLeuThrGlyIleAspThr 581
 QY 1915 ATACCACCTCAACGACTCAACAACTTTTCTGGTACAAATTATTAAT-----AATTTA 1968
 Db 582 IleSerValGlu---LeuProSerThrThrSerArgGlnAsnProAsnAlaThrAspLeu 600
 QY 1969 CAATACGGAGATTTTGGGTATTCCAAATTTCCAAGTACAGTA----- 2010
 Db 601 ThrTyrAlaAspPheGlyTyrValThrPheProArgThrValProAsnLysThrPheGlu 620
 QY 2011 -----ACNTACCTTTAATCGAACATACCATTTATTTAATTAATTCGTGCAGATGTA 2061
 Db 621 GlyGluAspThrLeuLeuMetThr-----LeuTyrGlyThrProAsnHis 635
 QY 2062 TCAAAATTCAAATTTAATCATTTGATAAATTTGAATTTATACCAATTTACTCTCTGACGC 2121
 Db 636 SerTyrAsnIle---TyrIleAspLysIleGluPheIleProIleThrGlnSerValLeu 654
 QY 2122 CAAATAGAGAGAAACAAATTAAGAACTATCCAAACAAATAAATACATTTTTCACA 2181
 Db 655 AspTyrThrGluLysGlnAsnIleGluLysThrGlnLysIleValAsnAspLeuPheVal 674
 QY 2182 AAT 2184
 Db 675 Asn 675
 RESULT 15
 ID ADR89431
 AC ADR89431 standard; protein; 675 AA.
 XX AC ADR89431;
 DT 18-NOV-2004 (first entry)
 DE cry10Aa.
 XX delta-endotoxin; delta-endotoxin associate polypeptide;
 KW expression cassette; transformation; transgenic; plant; bacteria;
 KW lepidoptera; coleoptera; pest; pesticide; resistance;
 KW pesticidal activity.
 XX Bacillus thuringiensis.
 OS WO2004074462-A2.
 PN 02-SEP-2004.
 PD 20-FEB-2004; 2004WO-US005829.
 XX 20-FEB-2003; 2003US-0448632P.
 PR 20-FEB-2003; 2003US-0448633P.
 PR 20-FEB-2003; 2003US-0448797P.
 PR 20-FEB-2003; 2003US-0448808P.
 PR 20-FEB-2003; 2003US-0448810P.
 PR 20-FEB-2003; 2003US-0448812P.
 PR 19-FEB-2004; 2004US-00781979.
 PR 19-FEB-2004; 2004US-00782020.

PR 19-FEB-2004; 2004US-00782096.
 PR 19-FEB-2004; 2004US-00782141.
 PR 19-FEB-2004; 2004US-00782570.
 XX 19-FEB-2004; 2004US-00783417.
 PA (ATHE-) ATHENIX CORP.
 XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
 XX WPI; 2004-635574/61.
 DR New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 XX and polypeptides, useful for killing lepidopteran or coleopteran pests or
 XX for producing organisms with pesticide resistance.
 XX Example 6; SEQ ID NO 43; 178pp; English.
 CC This sequence represents a delta-endotoxin crystal protein. This protein
 CC was included in the scope of the invention as a comparison to the delta-
 CC endotoxins of the invention. Some of the delta-endotoxin coding sequences
 CC of the invention have alternative start codons, producing more than one
 CC protein from a single open reading frame. The nucleic acid sequences of
 CC the invention are useful in DNA constructs or expression cassettes for
 CC transformation and expression in plants and bacteria. The nucleic acids
 CC and corresponding polypeptides are useful for killing lepidopteran or
 CC coleopteran pests. Compositions containing the delta-endotoxins of the
 CC invention, and methods for their production, are useful for the
 CC production of organisms with pesticide resistance, specifically bacteria
 CC and plants. These organisms are useful for generating altered or improved
 CC delta-endotoxin or delta-endotoxin-associated proteins that have
 CC pesticidal activity, or for detecting the presence of delta-endotoxin or
 CC delta-endotoxin-associated proteins or nucleic acids in products or
 CC organisms.
 XX SQ Sequence 675 AA;
 Alignment Scores:
 Pred. No.: 1.23e-66 Length: 675
 Score: 897.00 Matches: 251
 Percent Similarity: 47.96% Conservative: 114
 Best Local Similarity: 32.98% Mismatches: 268
 Query Match: 22.77% Indels: 128
 DB: 8 Gaps: 32
 US-10-782-570-1 (1-2235) x ADR89431 (1-675)
 QY 13 AATAAATAATGAATATGAGATTATCGATTCAAGAATTTATCTTATCTCTTCAACAGAAAT 72
 Db 6 AsnLysAsnGluTyrGluIlePheAsnAlaProSerAsnGlyPheSerLysSerAsnAsn 25
 QY 73 ATTGATCATTTCTAGATACCTTTACACAATAATCCAAATCAACATTTACAAACACAAAT 132
 Db 26 -----TyrSerArgTyrProLeuAlaAsnLysProAsnGlnProLeuLysAsnThrAsn 43
 QY 133 TACAAAGATGGCTCAATATGTCTCAGGGAATACACAATATGATGATATTTTCGAGACA 192
 Db 44 TyrLysAspTrpLeuAsnValCysGlnAspGlnGlnTyrGlyAsnAlaGlyAsn 63
 QY 193 TTTGCTAGTCTGATACAAATTTGCTGCAGGTAGTGCAGTACTATTGTCGGTACTCTG 252
 Db 64 PheAlaSerSerGluThrIleValGlyValSerAlaGlyIleIleValValGlyThrMet 83
 QY 253 TTAGCCGGTATAGTGGGCTCACTTCTATATCCGAGCCGATAGGAATAATAGTGCTGCTATA 312
 Db 84 LeuGly-----AlaPheAlaAlaPro-----ValLeuAlaAlaGly 95
 QY 313 ATAATATCTTTTGGTACCTTAATCACTGCTTTTGGCCCGGAGNACAGACAAACA 372
 Db 96 IleIleSerPheGlyThrLeuLeuProIlePheTrp---GlnGlySerAspProAlaAsn 114
 QY 373 GTATGGACACAAATTTTAAATAGGAGAAATTTTGTGTGATACACCGTTAAACAGAA--- 429
 Db 115 ValTrpGlnAspLeuAsnIleGly-----GlyArgProIleGlnGluIle 130

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QY 430 -----AGCATAAACAGCTAAAGTTCACAACTTTAGAGGATTTAGACAAATATTACAA 483
Db 131 AspLysAsnIleIleAsnValLeuThrSerIleValThrProIleLysAsnGluLeuAsp 150
QY 484 AGCTATAATACAGCATATAGATGATTGGAGAAAATTAATAAGACTACAAAGCTCCTGGATTA 543
Db 151 LysTyrGlnGluPheAspLysTrpGluProAlaArg ----- 163
QY 544 CCACATCATCAGCATATACAAACAGCTGCCCTTGACTCTTAATAATACGATTTGAGAAATGTT 603
Db 164 -----ThrHisAlaAsnAlaLysAlaValHisAspLeuPheThrThrLeuGluProIle 181
QY 604 CACAAAT-----GATTTTATTCGAGAAATACCTGGTTTCCAACTTGAACCTTATAAA 654
Db 182 IleAspLysAspLeuAspMetLeuLysAsnAsnAlaSerTyrArgIleProThr----- 199
QY 655 ACGCTATTACTACCTATTATGCGCAAGCTGCTCAATTTTCAATTTAAATTTATTACAACAA 714
Db 200 -----LeuProAlaTyrAlaGlnIleAlaThrTrpHisLeuAsnLeuLeuLysHis 216
QY 715 GGTGCTGAATGGCTGATGAATGAATGCAGATATACATCCTTCACAAATGAACCTTAAT 774
Db 217 AlaAlaThrTyrTyrAsnIleTrp-----LeuGlnAsnGlnGlyIleAsnProSer 233
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Db 462 TrpLys-----AsnGluGluTyrGlyHisThrLeu 471
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QY 1798 ATTACATGTAGA---ACTCCTTAATTTCTACACAATCTTTATTATACATTTAGACTTCGATACGCT 1854
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QY 2062 TCBAATTCAAATTTTAATCATTTGATAAAATTCGAATTTATACCAATTTACTTCTCTGTACGC 2121
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QY 2182 AAT 2184
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Search completed: January 12, 2006, 06:26:26
Job time : 235.5 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 12, 2006, 06:16:09 ; Search time 147 Seconds
(without alignments)

12705.422 Million cell updates/sec

Title: US-10-782-570-1

Perfect score: 3939

Sequence: 1 gtgaatcaaaataataa.....caaaactatgatattgattaa 2235

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2_1/USPTO.spool_p/US10782570/runat_12012006_060223_7574/app_query.fasta_1.2375
-DB=Published Applications AA Main -QFMT=fastan -SUFFIX=rapbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODS=LOCAL -OUTFMT=otc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10782570_@CEN_1_1_248_@runat_12012006_060223_7574
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Database :

Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3902	99.1	744	US-10-782-570-2	Sequence 2, Appl
2	3623	92.0	694	US-10-782-570-4	Sequence 4, Appl
3	3314	84.1	735	US-10-783-417-2	Sequence 2, Appl
4	1158	29.4	1180	US-10-782-141-12	Sequence 12, Appl
5	1158	29.4	1180	US-10-782-096-14	Sequence 14, Appl
6	1158	29.4	1180	US-10-782-570-10	Sequence 10, Appl
7	1158	29.4	1180	US-10-783-417-8	Sequence 8, Appl
8	1158	29.4	1180	US-10-781-979-14	Sequence 14, Appl
9	901	22.9	1109	US-09-756-526A-4	Sequence 4, Appl
10	901	22.9	1109	US-10-345-020-4	Sequence 4, Appl
11	901	22.9	1109	US-10-342-821-4	Sequence 4, Appl
12	897	22.8	675	US-10-782-141-17	Sequence 17, Appl

13	897	22.8	675	4	US-10-782-096-18	Sequence 18, Appl
14	897	22.8	675	4	US-10-782-570-14	Sequence 14, Appl
15	897	22.8	675	5	US-10-783-417-12	Sequence 12, Appl
16	897	22.8	675	5	US-10-781-979-19	Sequence 19, Appl
17	897	22.8	675	5	US-10-926-819-16	Sequence 16, Appl
18	819	20.8	1136	4	US-10-782-141-13	Sequence 13, Appl
19	819	20.8	1136	5	US-10-781-979-15	Sequence 15, Appl
20	819	20.8	1136	5	US-10-929-754-1	Sequence 1, Appl
21	716	18.2	1210	4	US-10-032-717-4	Sequence 4, Appl
22	716	18.2	1210	4	US-10-414-637-4	Sequence 4, Appl
23	716	18.2	1210	4	US-10-606-320-4	Sequence 4, Appl
24	716	18.2	1210	4	US-10-746-914-4	Sequence 4, Appl
25	709	18.0	682	4	US-10-782-096-20	Sequence 20, Appl
26	709	18.0	682	4	US-10-782-570-16	Sequence 16, Appl
27	709	18.0	682	5	US-10-783-417-14	Sequence 14, Appl
28	709	18.0	682	5	US-10-781-979-21	Sequence 21, Appl
29	708.5	18.0	780	6	US-11-018-615-29	Sequence 29, Appl
30	708.5	18.0	1169	6	US-11-018-615-25	Sequence 25, Appl
31	706	17.9	659	4	US-10-614-076-112	Sequence 112, App
32	706	17.9	659	4	US-10-782-096-12	Sequence 12, Appl
33	706	17.9	659	4	US-10-782-570-9	Sequence 9, Appl
34	706	17.9	659	5	US-10-783-417-7	Sequence 7, Appl
35	700	17.8	652	4	US-10-232-665-4	Sequence 4, Appl
36	700	17.8	652	4	US-10-614-076-110	Sequence 110, App
37	699	17.7	1206	4	US-10-032-717-2	Sequence 2, Appl
38	699	17.7	1206	4	US-10-414-637-2	Sequence 2, Appl
39	699	17.7	1206	4	US-10-606-320-2	Sequence 2, Appl
40	699	17.7	1206	4	US-10-746-914-2	Sequence 2, Appl
41	693	17.6	652	4	US-10-232-665-6	Sequence 6, Appl
42	691	17.5	652	4	US-10-232-665-2	Sequence 2, Appl
43	691	17.5	652	4	US-10-614-076-4	Sequence 4, Appl
44	691	17.5	652	4	US-10-614-076-10	Sequence 10, Appl
45	691	17.5	652	4	US-10-614-076-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1

US-10-782-570-2
; Sequence 2, Application US/10782570
; Publication No. US2004021096SAI
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Korziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and Methods for Its Use
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 744
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-2

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Score: 3902.00 Matches: 743
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.87% Mismatches: 0
Query Match: 99.06% Indels: 0
DB: 4 Gaps: 0

US-10-782-570-1 (1-2235) x US-10-782-570-2 (1-744)

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Db 21 SerAsnArgAsnIleAspHisSerArgTyrProTyrThrAsnAsnProAsnGlnProLeu 40
QY 121 CAAACACAAATTAACAAGAGTGGCTCAATATGTCTCAAGGAAATACACATATGGTGAT 180
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QY 481 CAAGCTATATACAGCATAGATGATTTGGAGAAAAATTTAAAGACTACAGCTCCTGGA 540
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; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-4
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 91.98% Indels: 0
DB: 4 Gaps: 0
US-10-782-570-1 (1-2235) x US-10-782-570-4 (1-694)
QY 151 ATGTCTCAAGGGAATACAAATATGGTGAATAATTCGAGACATTTGCTAGTCTGATACA 210
Db |||||
1 MetCysGlnGlyAsnThrGlnTyrGlyAspAsnPheGluThrPheAlaSerAlaAspThr 20
QY 211 ATTTGTCGATTTAGTCAGGACTATTGCTCGCTACTCTCTGCTAGTCTGCTAGTCTGCTG 270
Db |||||
21 IleAlaAlaValSerAlaGlyThrIleValSerGlyThrLeuLeuAlaGlyIleGlyGly 40
QY 271 CTCACCTCTATATCCGACCGCATAGGAATAATAGGTGCTATATAATATCTTTTGTGCTACC 330
Db |||||
41 LeuThrSerIleSerGlyProIleGlyIleGlyIleGlyAlaIleIleSerPheGlyThr 60
QY 331 CTAATCAGTCTTTTGGCCCGGAGAACAGACAAACAGTATGGACACAAATTTAT 390
Db |||||
61 LeuIleThrValPheThrProIleGlyGluGlnAspLysThrValTrpThrGlnPheIle 80
QY 391 AAAATGGGAGAAATTTTGTGATACACCGTTAAACAGAGCATAAACAGCTAAAGTTA 450
Db |||||
81 LysMetGlyGluIlePheValAspThrProLeuThrGluSerIleLysGlnLeuLysLeu 100
QY 451 CAAACTTTAGAGGATTTAGACAAATATTAACAAAGCTATAATACAGCATTAGATGTTGG 510
Db |||||
101 GlnThrLeuGluGlyPheArgGlnIleLeuGlnSerTyrAsnThrAlaLeuAspThrP 120
QY 511 AGAAAAATTAAAGACTCAAGCTCTCGATTACCAACCATCATCAGCATTACAAAGCT 570
Db |||||
121 ArgLysLeuLysArgLeuGlnAlaProGlyLeuProProSerSerAlaLeuGlnAla 140
QY 571 GCCTTCAGCTTAAATACGATTTGAGATGTTTCAATGATTTTATTCAGAAATACCT 630
Db |||||
141 AlaLeuThrLeuLysIleArgPheGluAsnValHisAsnAspPheIleArgGluIlePro 160
QY 631 GGTTCCTCAACTTATAAAACGCTATTACTACTATTATTTATCGCGAAGCTGCTAAT 690
161 GlyPheGlnLeuGluThrTyrLysThrLeuLeuLeuProIleTyrAlaGlnAlaAsn 180
691 TTTTCATTTAAATTTATTACAAAGGTGCTGAATTTGGCTGATGAATGAATGACAGATATA 750
181 PheHisLeuAsnLeuLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 200
751 CATCTTTCACAAATTTGAACCTAAATGCTGGAAACATCAGATGACTATTATAAACTTTTAAA 810
201 HisProSerGlnIleGluProAsnAlaGlyThrSerAspAspTyrTyrLysLeuLeuLys 220
811 GAAATATACCTAATATATAGTAATATTGTCGCAATACCTATAGAGAGGAGGCTAAATAAA 870
221 GluAsnIleProLysTyrSerAsnTyrCysAlaAsnThrTyrArgGluGlyLeuAsnLys 240
871 CTTCGAAACGAACTAATATAGAGTGGATATATTAAATGATATATCGAAGATATATGACT 930
241 LeuArgAsnGluProAsnMetArgTrpSerIlePheAsnAspTyrArgArgTyrMetThr 260
931 ATTACTGTATTAGATACCTATCGCTCAATTTTCTTTTATGATATATAAGAGATACAAAGAT 990
261 IleThrValLeuAspThrIleAlaGlnPheSerPheTyrAspIleLysArgTyrLysAsp 280
991 TCAATAGGAAAGATAGGTGGCAATTAAACTGAACCTTACAAGAGAAATTTATACAACTGAA 1050
281 SerIleGlyArgIleGlyIleLysThrGluLeuThrArgGluIleTyrThrThrGlu 300
1051 ATAAATTTTGACCTCTTACTTACCTTGAAATTCACCCCAATCTCGCTATATATGCAATAT 1110
301 IleAsnPheAspArgLeuThrTyrLeuGluIleGlnProAsnLeuAlaIleMetGluTyr 320
1111 AATTTAACACGCTTCAGGGCTTAGATATTATTTTCAATTTTATGATGAACTTATTTTATACA 1170
321 AsnLeuThrArgSerGlyLeuArgLeuPheSerPheLeuAspGluLeuIlePheTyrThr 340
1171 AAAAATGAAACGTACGGGAATCGTTTACTGCTATGCGAATCGAATGCTAATGATCTACTAT 1230
341 LysAsnGluThrTyrGlyAsnArgLeuValGlyIleAlaAsnArgAsnArgSerThrTyr 360
1231 GCTACGACGAACTGAAATTTATATATGAGAAAGAACAGGTCCACCCACCAACAAACT 1290
361 AlaThrThrGlyThrGluIleIleTyrGlyGluArgThrGlyProProThrThrLysThr 380
1291 TTAATACCATTTGATCTTATAAGTTTCAATTTGTAACGTAGTACAGCAAGTACTCTACT 1350
381 LeuIleProPheGluSerTyrLysValSerIleValThrAspArgGlnValThrProThr 400
1351 TCCCTTTTCTTAACATATATCTTCAATTAATCAAAATGAACTTTTATTAATTAATTCAC 1410
401 SerProPheProAsnIleTyrPheThrIleAsnGlnIleGluLeuTyrLeuAsnAsnSer 420
1411 CCTAGTAATAATTAACATATATTCAGCTGGGGGGAATTTATCTAATGATAAAAAACAAC 1470
421 ProSerAsnLysLeuThrTyrSerAlaGlyAsnLeuSerAsnAspLysLysThrThr 440
1471 GATTTTCAATTTCTGTAAAAAAGACTGTAAACCAATTTATTAATCCAAATTTGTTTACCA 1530
441 AspPheGlnPheProValLysLysAspCysLysProIleLeuAsnProAsnCysLeuPro 460
1531 AGCTATAATAGTATTAGTCATATTTTATCCAGTTTCTTTTCTTTTATTAATTTCTCTATAAA 1590
461 SerTyrAsnSerTyrSerHisIleLeuSerGlnPheSerLeuPheAsnTyrSerTyrLys 480
1591 ATTGATTTAGCGCTAAATATATATATATATACGTGTCATTTAGGATGACACACAGTAGTGT 1650
481 IleGlyLeuAlaLeuAsnIleLeuTyrThrGlyAlaLeuGlyTrpThrHisSerVal 500
1651 AATGAAATTAATGCAATATCAGATAAAATAATTAATATGATATCCAGCAATCAAAGTAC 1710
501 AsnArgAsnAsnAlaIleSerAspLysIleIleThrMetIleProAlaIleLysGlyAsn 520
1711 AGTCTTGATACAACTCTAAGGTAATTAAGGACCTGCTGCTATATCGAGGAAACTTGGTT 1770
```

Db 521 SerLeuAspThrAsnSerLysValIleGluGlyProGlyHisThrGlyGlyAsnLeuVal 540
QY 1771 TATTACAAAGTCAAGGGCGTTTAGAGATTACATGTAGAACTCCCTAAATCTTACACAATCT 1830
Db 541 TyrLeuGlnSerGlnGlyArgLeuGluIleThrCysArgThrProAsnSerThrGlnSer 560
QY 1831 TATTACATTAGACTTCGATACCTCAAAATGGTGTGGAAATACATCTTCCCTAATATATCT 1890
Db 561 TyrTyrIleArgLeuArgTyrAlaThrAsnGlyAlaGlyAsnThrLeuProAsnIleSer 580
QY 1891 CTTTCAATACCAAGGAGTAAATAGGATACCACTTCAACGACTCAACCAACACTTTTCTCGT 1950
Db 581 LeuThrIleProGlyValIleGlyIleProGlnArgLeuAsnAsnThrPheSerGly 600
QY 1951 ACAATATAATAATTAACAATACCGAGATTTGGGTATTTCCATTTTCCAAAGTACAGTA 2010
Db 601 ThrAsnTyrAsnAsnLeuGlnTyrGlyAspPheGlyTyrPheGlnPheProSerThrVal 620
QY 2011 ACATTACCTTTAAATCGAAACATACCATTTATATTAATCGTGCAGATGTATCAAAATCA 2070
Db 621 ThrLeuProLeuAsnArgAsnIleProPheIlePheAsnArgAlaAspValSerAsnSer 640
QY 2071 ATTTTAATCATTGATAAAATTTGAATTTATATCAATTTACTTCTCTGTAGGCCAAATAGA 2130
Db 641 IleLeuIleIleAspLysIleGluPheIleProIleThrSerSerValArgGlnAsnArg 660
QY 2131 GAAAAACAAAATTAAGAACTATCCAAACAAAATAAATACATTTTTCACAAAATCATACA 2190
Db 661 GluLysGlnLysLeuGluThrIleGlnThrLysIleAsnThrPhePheThrAsnHisThr 680
QY 2191 AAAATACCTTTAAATPATAGAGCCCAAACTATGATATTGAT 2232
Db 681 LysAsnThrLeuAsnIleGluAlaThrAsnTyrAspIleAsp 694

RESULT 3

US-10-783-417-2
; Sequence 2, Application US/10783417
; Publication No. US20040216186A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziele, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-006, A Delta-Endotoxin Gene and
; FILE REFERENCE: Methods for Its Use
; CURRENT APPLICATION NUMBER: US/10/783,417
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,806
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-783-417-2

Alignment Scores:

Pred. No.: 3,49e-265 Length: 735
Score: 3314.00 Matches: 638
Percent Similarity: 91.28% Conservative: 32
Best Local Similarity: 86.92% Mismatches: 60
Query Match: 84.13% Indels: 4
DB: 5 Gaps: 3

US-10-782-570-1 (1-2235) x US-10-783-417-2 (1-735).

QY 1 GTGAATCAAATAT---AATTAAGATATAGATTATCGATTCAAGAAATTTATCTTAT 57
:::|||||
Db 1 MetAsnGlnAsnAsnAspAsnAsnGluTyrGluIleIleAspSerHisThrSerProTyr 20
|||

QY 58 CTTTCTAACAGAAATATTGATCATTTCTAGATACCTTTACACAATAATATCCAAATCAACCA 117
Db 21 PheProAsnArgAsnSerAsnAspSerArgTyrProTyrThrAsnAsnProAsnGlnPro 40
:::
QY 118 TTACAAAACACAAATTAACAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGT 177
Db 41 LeuGlnAsnThrAsnTyrLysGluTyrLeuAsnMetCysGlnGlyAsnThrGlnTyrGly 60
QY 178 GATAATTTCCAGACATTTGCTAGTGTGATACAAATTCGCTCAGTGTAGTGCAGGTACTATT 237
Db 61 AspAsnPheGluThrPheAlaSerAlaAspThrIleAlaAlaValSerAlaGlyThrIle 80
QY 238 GTATCCCGTACTCTGTTAGCCGGTATAGTGGGCTCACTTCTATATCCGACCCATAGGA 297
Db 81 ValSerGlyThrLeuLeuAlaGlyIleGlyGlyLeuThrSerIleSerGlyProIleGly 100
QY 298 ATAATAGTCTATAATAATATCTTTTGGTACCTTAATCACTGTCTTTTGGCCCGCGGA 357
Db 101 IleIleGlyAlaIleIleSerPheGlyThrLeuIleThrValPheTyrProAlaGly 120
QY 358 GAACACAGACAAAACAGTATCGACACAATTTTAAATGGAGAAAATTTTGTGTATACA 417
Db 121 GluGlnAspLysThrValTyrThrGlnPheIleLysMetGlyGluIlePheValAspThr 140
QY 418 CCGTTAACAGAAAGCATAAACAGCTAAAGCTTACAACTTTAGAGGATTTAGACAATA 477
Db 141 ProLeuThrGluSerIleLysGlnLeuLysLeuGlnThrLeuGluGlyPheArgGlnIle 160
QY 478 TTCAAAGCTATTAATACAGCATTTAGATGTGGAGAAAATTTAAAAAGACTACAGCTCCT 537
Db 161 LeuGlnSerTyrAsnThrAlaLeuAspAspTyrArgLysLeuLysArgLeuGlnAlaPro 180
QY 538 GGATTACCAACCATCATCAGCATTTACACAAGCTGCCTTGACTCTTAAATAATCATTTGAG 597
Db 181 GlyLeuProProSerSerAlaLeuGlnGlnAlaLeuThrLeuLysIleArgPheGlu 200
QY 598 AATGTTCAACAATGATTTTATTCAGAGAAATACCTGGTTCCAACTTCAAACTTATAAACG 657
Db 201 AsnValHisAsnAspPheIleArgGluIleProGlyPheGlnLeuGluThrTyrLysThr 220
QY 658 CTATTACTACTATTTATGCGCAAGCTGCTAATTTTTCATTTAAATTTATTACAAAGGT 717
Db 221 LeuLeuLeuProIleTyrAlaGlnAlaAlaAsnPheHisLeuAsnLeuLeuGlnGly 240
QY 718 GCTGAATTTGGCTGATCAATGGAATGCAGATATACATCCTTCAACAATTTGAACCTATGCT 777
Db 241 AlaGluLeuAlaAspGluTyrAsnAlaAspIleHisProSerGlnIleGluProAsnAla 260
QY 778 GGAACATCAGATGACTATTATAAACTTTTAAAGAAAATATACCTAAATATAGTAACTAT 837
Db 261 GlyThrSerAspAspTyrTyrLysLeuLeuLysGluAsnIleProLysTyrSerAsnTyr 280
QY 838 TGTGCAAAATACCTATAGAGAGGACTAAATAAACTTCGAAACGAACTATATATGAGATGG 897
Db 281 CysAlaAsnThrTyrArgThrGlyLeuLysAsnLeuArgAspGluProAsnMetLysTip 300
QY 898 AGTATATTAAATGATTTATCGAAGATATATGACTATTTACTGTATATAGTACTATCGCTCAA 957
Db 301 SerIlePheAsnAspTyrArgArgTyrMetThrIleThrValLeuAspThrIleSerGln 320
QY 958 TTTTCTTTTATGATATAAGAGATACAAAGATTCAATAGGA-----AGAATAGGTGGC 1011
Db 321 PheSerLeuTyrAspIleLysArgTyrArgAspSerIleGlyIleGluValLysGly 340
1012 ATTTAAACCTGAACCTTACAAGAGAAAATTTATACAACCTGAATAAATTTTGCACCGCTTACT 1071
Db 341 IleLysAsnGluLeuThrArgGluIleTyrThrGluIleAsnPheAspArgLeuPro 360
1072 TACCTTGAATTCACCCCAATCTCGCTATATATGGAATATAATTTAAACAGTTCAGGGCTT 1131
Db 361 GlnLeuArgValGlnProAsnLeuAlaThrMetGluTyrAsnLeuThrArgAlaSerPhe 380
:::
1132 AGATTATTTTCTATTTAGATGACTTATATTTTATACAAAATAATGAAACGTACGGGAAT 1191

Db 681 ileArgGluAspArgGluLysGlnLysLeuGluThrValGlnGlnIleleasnThrPhe 700
QY 2176 TTCACAAATCATACAAAAATCTTTAAATATAGAGCCACAACTATGATTCAT 2232
Db 701 TyrAlaAsnProIleLysAsnThrLeuGlnSerGluLeuThrAspTyrAspIleAsp 719

RESULT 6

US-10-782-570-10
; Sequence 10, Application US/10782570
; Publication NO. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Teacy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-10

Alignment Scores:

Pred. No.:	7,86e-87	Length:	1180
Score:	1158.00	Matches:	283
Percent Similarity:	54.5%	Conservative:	131
Best Local Similarity:	37.29%	Mismatches:	281
Query Match:	29.40%	Indels:	64
DB:	4	Gaps:	25

US-10-782-570-1 (1-2235) x US-10-782-570-10 (1-1180)

QY 13 AATAATAATGAATGAGATTATCGATTCA-----AAGAAATTTATCTTCTCTTAAC 66
Db 6 AsnLysAsnGluTyrGluThrLeuAsnAlaSerGlnLysLeuAsnIleSerAsnAsn 25
QY 67 AGAAATATTGATCATCTTAGATACCTTACACAAATATCCAAATCAACCATTTACAAAC 126
Db 26 -----TyrThrArgTyrProIleGluAsnSerProLysGlnLeuLeuGlnSer 41
QY 127 ACBAATTTACAAGATGGCTCAATATGTCTCAGGGAAATACACATATGGTGATAATTC 186
Db 42 ThrAsnTyrLysAspTyrLysAsnMetCysGlnGlnAsnGlnGlnTyrGlyLysAspPhe 61
QY 187 GAGACATTTGCTAGTGTGATACAAATTCGCTGAGTGTAGTGTAGTGTATGTCGGT 246
Db 62 GluThrPheIleAspSer-----GlyGluLeuSerAlaTyrThrIleValGly 78
QY 247 ACTCTGTTAGCGGFPATAGTGGGCTCACTTCTATATCCGGACCGATAGGAATAATAGT 306
Db 79 ThrValLeuThrGlyPheGlyPheThrThr-----ProLeuGlyLeu----- 92
QY 307 GCTATAATAATATCTTTGGTACCTTAATCTACTGTCTTTGGCGCGGGAGACACAGAC 366
Db 93 ---AlaLeuIleGlyPheGlyThrIleuIleProValLeuPheProAlaGlnAspGlnSer 111
QY 367 AAAACAGTATGACACAAATTTATTAATAATGGAGAAATTTTGTGTATACACCGTTAACA 426
Db 112 AsnThr---TrpSerAspPheIleThrGlnThrLysAsnIleIleLysLysGluIleAla 130
QY 427 GAAAGCATAAACAGCTAAAGTTACAAACTTTAGAGGATTTAGACAAATATTACAAAGC 486
Db 131 SerThrTyrIleSerAsnAlaAsnLysIleLeuAsnArgSerPheAsnValIleSerThr 150

QY 487 TATAATACAGCATTTAGATGATTCGAGAAAATTAATAAAGACTACAGCTCCTGGATTACCA 546
Db 151 TyrHisAsnHisLeuLysThrTrpGlu-----AsnAsnProAsnProGln 165
QY 547 CCATCATCAGCATTTACACAAAGCTCGCTTGAATCTTAAATATACGATTTGAGAATGTTCCAC 606
Db 166 AsnThrGlnAspValArgThrGlnIleGlnLeuValHisTyrHisPheGlnAsnValIle 185
QY 607 AATGATTTTATTCGAGAAATACCT-----GGTTTCCAACCTTGAACTTTATAAAACGCTA 660
Db 186 ProGluLeuValAsnSerCysProAsnProSerAspCysAspTyrTyrAsnIleLeu 205
QY 661 TTACTACTATTATTCGCAAGCTGCTAATTTTCAATTTTAAATTTTATTAACAACAGGTGCT 720
Db 206 ValLeuSerSerTyrAlaGlnAlaAlaAsnLeuHisLeuThrValLeuAsnGlnAlaVal 225
QY 721 GAATTCGCTGATGAATGGAATGCAGATATACATCTTCAAAATTTGAACCTTAATGCTGGA 780
Db 226 LysPheGluAlaTyrLeuLysAsnAsnArgGlnPheAspTyrLeuGluPro---LeuPro 244
QY 781 ACATCAGATGACTATTATAAATCTTTTAAAGAAAATATATACCTAAATATAGTAATATTGT 840
Db 245 ThrAlaIleAspTyrTyrProValLeuThrLysAlaIleGluAspTyrThrAsnTyrCys 264
QY 841 GCAATACCTTATAGAGAGGACTAAATAAATCTTCAAAACGAACT----- 885
Db 265 ValThrThrTyrLysLysGlyLeuAsnLeuIleLysThrThrProAspSerAsnLeuAsp 284
QY 886 ---AATATGAGATGGAGTATATTAATGATTATCGAAGATATATGATCTATTACTGTATTA 942
Db 285 GlyAsnIleAsnTrpAsnThrTyrAsnThrTyrArgThrLysMetThrThrAlaValLeu 304
QY 943 GATACTATCGCTCAATTTCTTTTATGATATAAGAGATACAAAGATCATAAGTCAATAGGAAGA 1002
Db 305 AspLeuValAlaLeuPheProAsnTyrAspValGlyLysTyrProIle----- 320
QY 1003 ATAGTGTGCATTTAAACTGACTTACAGAGAAATTTTATACACTGAAATAAATTTTGAC 1062
Db 321 -----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal---LeuAsnPheGlu 337
QY 1063 CGTCTTACTTACCTTGAATTTCAACCAATCTCGCTATAATGGAATATAATTTTAAACAGT 1122
Db 338 GluSerProTyrLysTyrTyr-----AspPheGlnTyrGlnGluAspSerLeuThrArg 355
QY 1123 TCAGGGCTTAGATATTCTTCAATTTTAGTAGAATATATTTTATACAAAAATGAAACG 1182
Db 356 ArgPro---HisLeuPheThrTrpLeuAspSerLeuAsnPheTyrGluLysAlaGlnThr 374
QY 1183 TACGGGAATCGTTAGTGTGATTCGGAATCGTAATAGATCTACTTATGCT----- 1233
Db 375 ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn 393
QY 1234 ACACAGGAATCGAAATATATATATGAGAAAGAACAGCTCCACCCACACAAAAACTTTA 1293
Db 394 IleSerGlnLysSerSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu 413
QY 1294 ATACATTTGAATTCCTATAAAGTTTCAATTTGTAATGATAGACAAAGTAATCTTCTTCC 1353
Db 414 -----GlyLeuAlaThrAsnIleTyrIlePheLeuLeuAsnValIleSerLeuAspAsn 431
QY 1354 CTTTTTCTTAACATATCTTTACATTAATCAATTTGAATCTTATTTTAAATATTCACCT 1413
Db 432 LysTyrLeuAsnAspTyrAsnAsnIleSerLysMetAspPhePheIleThrAsnGlyThr 451
QY 1414 -----AGTAATAATTAACATATTTCAGCTGGGGGAATTTATCTAATGATAAAAAA 1464
Db 452 ArgLeuLeuLysGluLeuThr---AlaGlySerGlyGlnIleThrThrAspValAsn 470
QY 1465 ACAACTGATTTTCAATTTCTGTAAAAAAAGACTGTAAACCAATATTATTAATCCAAATGT 1524
Db 471 LysAsnIlePheGlyLeuProIleLeuLysArgArgGluAsnGlnGlyAsnProThrLeu 490

QY	943	GATAC	TACGCTCAATTTCTTTTATCATATAAAGACATACAAGATTCAATAGGAGA	1002
Db	305	AspLeu	ValAlaLeuPheProAsnTyrAspValGlyIstyrProIle	320
QY	1003	ATAGT	GGCCATTAACACTTACAGAGAAATTTATACAACCTGGAATATAATTTTAC	1062
Db	321	-----	GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal---LeuAsn	337
QY	1063	CGTCT	TACTTACCTTGAATAACACCAATCTCGCTATAATGGAAATATAATTTAACACGT	1122
Db	338	GluSerPro	TyrLysTyrTyr-----AspPheGlnTyrGlnGluAspSerLeuThrArg	355
QY	1123	TCAGG	CTTAGATATTTTCATTTTAGATGAACCTTATATTTTATACAAAATGAAACG	1182
Db	356	ArgPro	-----HisLeuPheThrTrpLeuAspSerLeuAsnPheTyrGluLysAlaGlnThr	374
QY	1183	TACGG	GAATCGCTTGTAGTTGGTATTTGCCGAATCGTAATAGACTCTATTGCT	1233
Db	375	ThrPro	AsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn	393
QY	1234	ACGAC	GAGNACTGAATATATATATGGAGAAAGACAGCTCCACCAACAACAAACTTTA	1293
Db	394	IleSerGln	LysSerSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu	413
QY	1294	ATACC	ATTGGAATCCTATAAAGTTTCAATTTGTAAGTACTGATAGACAAGTAACTCCTACTTCC	1353
Db	414	-----	GlyLeuAlaThrAsnIleTyrIlePheLeuLeuAsnValIleSerLeuAspAsn	431
QY	1354	CTTTT	CTCATACATATCTTTACAAATAATGCAACTTTATTAATAATAATTTCACTT	1413
Db	432	LysTyr	LeuAsnAspTyrAsnAsnIleSerLysMetAspPhePheIleThrAsnGlyThr	451
QY	1414	-----	ACTAATAAATTAACATATTCAGCTGGGGGAATTTATCTAATGATAAAAA	1464
Db	452	ArgLeu	LeuGluLysGluLeuThr---AlaGlySerGlyGlnIleThrTyrAspValAsn	470
QY	1465	ACRAC	TGATTTTCAATTTCTCGTAAAAAAGACTGTAAACCAATTTATATCCAAATGT	1524
Db	471	LysAsn	IlePheGlyLeuProIleLeuLysArgGluAsnGlnGlyAsnProThrLeu	490
QY	1525	TTACA	AGCTATATAGTTATAGTATAGTATATTTATCCAGTTTCTTTATTTAATATAT	1581
Db	491	PhePro	ThrTyrAspAsnTyrSerHisIleLeuSerPheIleLysSerLeuSerIlePro	510
QY	1582	---TC	CTATAAAATTTGGATTAGCCCTAAAATATATATATATACAGTGCATTTAGATGACA	1638
Db	511	AlaThr	TyrLys-----ThrGlnValTyrThrPheAla-----TrpThr	523
QY	1639	CACAG	TAGTGTATATAGAAATAATGCAATATCAGATAAAATAATTAATGATCCACGA	1698
Db	524	HisSer	ValAspProLysAsnThrIleTyrThrHisLeuThrThrGlnIleProAla	543
QY	1699	ATCAA	AGGTAAACAGTCTTGTATACAAACTTAAAGTAAATTCGAAGCACTGCTCATACAGGA	1758
Db	544	ValLys	AlaAsnSerLeuGlyThrAlaSerLysValValGlnGlyProGlyHisThrGly	563
QY	1759	GGAA	CTTGTATTTTACAAGTCAAGGGCGTTTAGAGATTACATGATAGAACTCCTAAT	1818
Db	564	GlyAsp	LeuIle-----AspPheLysAspPhePheLysIleThrCysGlnHisSerAsn	581
QY	1819	TCTAC	CAACTCTTATTACATTTAGATTCGATACGCTACAAATCGTCTCGAATATCTCT	1878
Db	582	PheGln	GlnSerTyrPheIleArgIleArgTyrAlaSerAsnGlySerAlaAsnThrArg	601
QY	1879	CCTAA	TATATCTCTTACAATAACGAGGAGTAAATAGGAATACCACTCAACGACTCAACAAC	1938
Db	602	AlaVal	IleAsnLeuSerIleProGlyValAlaGluLeu---GlyMetAlaLeuAsnPro	620
QY	1939	ACTTT	TCTCGTACAAATATATATATTTACAATACGAGATTTTGGGTATTTTCCAAATTT	1998
Db	621	ThrPhe	SerGlyThrAspTyrThrAsnLeuLysTyrLysAspPheGlnTyrLeuGluPhe	640

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QY 1999 CCAAGTACGTAACATTCACCTTTAAATCGAAACATACCACATTATATATTTAATCTGTGCAGAT 2055
Db   :::: |||
641 SerAsnGluValIysPheAlaProAsnGlnAsnIleSerLeuValPheAsnArgSerAsp 660
QY 2059 GTA---TCAAATTCAAATTTAAATCATTCGTATAAAATTCGAATTTTATACCAATTACTTCTCT 2115
Db   ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: |||
661 ValTyrThrAsnThrValLeuIleAspIleAspIleGluPheLeuProIleThrArgSer 680
QY 2116 GTACGCCAAATATAGAGAAAAACAAAATATAGAACTATATCCAAACAAAAATAAATACATTT 2175
Db   :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: |||
681 IleArgGluAspArgGluIysGlnIysLeuGluThrValGlnGlnIleAsnThrPhe 700
QY 2176 TTCACAATCATACAAAAATACCTTTAAATATAGAGCCACCAAACTATGATTTGAT 2232
Db   :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: |||
701 TyrAlaAsnProIleIysAsnThrLeuGlnSerGluLeuThrAspTyrAspIleAsp 719

RESULT 8
US-10-781-979-14
; Sequence 14, Application US/10781979
; Publication No. US2004025031A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMT-008, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-781-979-14

Alignment Scores:
Pred. No.: 7,86e-87 Length: 1180
Score: 1158.00 Matches: 283
Percent Similarity: 54.55% Conservative: 131
Best Local Similarity: 37.29% Mismatches: 281
Query Match: 29.40% Indels: 64
DB: 5 Gaps: 25

US-10-782-570-1 (1-2235) x US-10-781-979-14 (1-1180)
QY 13 AATAATAATGAATATCAGATTATCGATTCA-----AGAAATTTATCTTATCTTCTTAAC 66
Db   ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: |||
6 AsnIleAsnGluTyrGluThrLeuAsnAlaSerGlnIysLeuAsnIleSerAsnAsn 25
QY 67 AGAAATATTGATCATTTCTAGATACCCCTTACACAAATATATCCAAATCAACCAATTACAAAAC 126
Db   :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: |||
26 -----TyrThrArgTyrProIleGluAsnSerProIysGlnLeuLeuGlnSer 41
QY 127 ACAAAATTACAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGTGATTAATTC 186
Db   ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: |||
42 ThrAsnTyrIysAspTrpLeuAsnMetCysGlnGlnAsnGlnIleGlyGlyAspPhe 61
QY 187 GAGACATTTGCTAGTCTGCTGATACAAATTCGTGCGAGTTAGTGCAGGTACTATTGTTATCCCGT 246
Db   ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: |||
62 GluThrPheIleAspSer-----GlyGluLeuSerAlaTyrThrIleValValGly 78
QY 247 ACTCTGTGTAGCCGTATAGTGGGCTCACTTCTATATCCGACCCATAGGAAATAATAGT 306
Db   ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: |||
79 ThrValLeuThrGlyPheGlyPheThrThr-----ProGlyGlyLeu----- 92
QY 307 GCTATAATAATATCTTTTTCGGTACCCCTAATCACTGTCCTTTTCCGCCCGCGGAGAACAC 366
Db   :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: ||| :::: |||

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Db 93 ---AlaLeuIleGlyPheGlyThrLeuIleProValLeuPheProAlaGlnAspGlnSer 111
Qy 367 AAACAGATATGACACAAATTTATTAATGGAGAAATTTTGTGTATACACCGTTAACA 426
Db 112 AenThr---TrpSerAspPheIleThrGlnThrLysAenIleIleLysGluIleAla 130
Qy 427 GAAAGCATAAACACAGCTAAAGTTACAACTTTAGAGAGATTAGACAAATTTATACAAAGC 486
Db 131 SerThrTyrlleSerAsnAlaAsnLysIleLeuAenArgSerPheAsnValIleSerThr 150
Qy 487 TATAATACAGCATATAGATGTTGGAGAAATTTAAAGACTACAAAGCTCCCTGGATTACCA 546
Db 151 TyrHisAenHisLeuLysThrTrpGlu-----AsnAsnProAsnProGln 165
Qy 547 CCATCATCAGCATTAACAACAGCTGCCTTGACTCTTTAAATACGATTGTGAGATGTTCCAC 606
Db 166 AenThrGlnAspValArgThrGlnIleGlnLeuValHisTyrHisPheGlnAsnValIle 185
Qy 607 AATGATTTTATTCGAGAAATACCT-----GTTTCCAACTTTGAAACTTATAAAACGCTA 660
Db 186 ProGluLeuValAsnSerCysProProAsnProSerAspCysAspTyrTyraenIleLeu 205
Qy 661 TTACTACTATTATATGCGCAAGCTGCTAATTTTCATTTTAAATTTATTAATTAACAAGTGCT 720
Db 206 ValLeuSerSerTyrAlaGlnAlaAlaAenLeuHisLeuThrValLeuAenGlnAlaVal 225
Qy 721 GNAITGGCTGAATGGAATGCAGATATACATACCTTCCAAATTTGAACCTTAATGCTGGA 780
Db 226 LysPheGluAlaTyrLeuLysAenAsnArgGlnPheAspTyrLeuGluPro---LeuPro 244
Qy 781 ACATCAGATGACTATTATTAATCTTTAAAGAAATATATACCTTAATATAGTAATCTTGT 840
Db 245 ThrAlaIleAspTyrTyrProValLeuThrLysAlaIleGluAspTyrThrAsnTyrCys 264
Qy 841 GCAATATCTATPAGAGAGAGCTAATAAATCTTCGAAACGAACT----- 885
Db 265 ValThrTyrLysGlyLeuAenLeuIleLysThrProAspSerAsnLeuAsp 284
Qy 886 ---AATATCAGATGAGTATATTTAATGNTATCGAAGATATATACATATCTACTATTA 942
Db 285 GlyAenIleAsnTrpAsnThrTyrAsnThrTyrArgThrLysMetThrThrAlaValLeu 304
Qy 943 GATACCTATCGCTCAATTTCTTTTATGATATATAAGAGATACAAAGATTCATAGAGA 1002
Db 305 AspLeuValAlaLeuPheProAsnTyrAspValGlyLysTyrProIle----- 320
Qy 1003 ATAGTGGCATTAATACTGAACCTTACAGAGAAATTTATPACAACTGAAATAATTTGAC 1062
Db 321 -----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal---LeuAenPheGlu 337
Qy 1063 CGTCTTACTTACCTTGAAATTCACCAATCTCGCTATTAATCGATATATTAATTAACAGCT 1122
Db 338 GluSerProTyrLysTyrTyr-----AspPheGlnTyrGlnGluAspSerLeuThrArg 355
Qy 1123 TCAGGCTTAGATATTTTTCATTTTATGTAAGTATATATTTATACAAATAATGAAACG 1182
Db 356 ArgPro---HisLeuPheThrTrpLeuAspSerLeuAenPheTyrGluLysAlaGlnThr 374
Qy 1183 TAGGGAATCGTTAGTGTGTAATCGAATCGTAATPAGATCTACTTATCT----- 1233
Db 375 ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn 393
Qy 1234 ACAGAGGAAGCTGAATTTATATATGGAAGAGAACAGGTCCACCCACAAACAACTTTA 1293
Db 394 IleSerGlnLysSerSerValPheGlyAenHisAenValThrAspLysLeuLysSerLeu 413
Qy 1294 ATACCATTTGAATCTTAAGATTTCATTTGTAATCTGATAGACAGTAATCTCTACTCT 1353
Db 414 -----GlyLeuAlaThrAenIleTyrIlePheLeuLeuAenValIleSerLeuAspAsn 431
Qy 1354 CCTTTTCTAACATATCTTACAAATTAATCAATTAATCAATTTATTAATTAATCACT 1413
Db 432 LysTyrLeuAenAspTyrAsnAenIleSerLysMetAspPheIleThrAenGlyThr 451

Qy 1414 -----AGTATAAATTAACATATTCAGCTGGGGGAATTTATCTAATGATAAAAAA 1464
Db 452 ArgLeuLeuGluLysGluLeuThr---AlaGlySerGlyGlnIleThrTyrAspValAsn 470
Qy 1465 ACAACTGATTTTCATTTCTGTAAAAAGACGTGTAAACCAATTTATTAATCCAATTTGT 1524
Db 471 LysAenIlePheGlyLeuProIleLeuLysArgArgGluAenGlnGlyAsnProThrLeu 490
Qy 1525 TTACCAAGCTATATAGTATAGTATATTTATCCAGTTTCTTTTATTAATATAT--- 1581
Db 491 PheProThrTyrAspAsnTyrSerHisIleLeuSerPheIleLysSerLeuSerIlePro 510
Qy 1582 ---TCCTATAAATTTGAGTTAGCCCTAAATATATATATATATATATATAGGTGATAGGAC 1638
Db 511 AlaThrTyrLys-----ThrGlnValTyrThrPheAla-----TyrThr 523
Qy 1639 CACAGTAGTGTATAGAAATATGCAATATACATATAAATAATATATATATATATATATAT 1698
Db 524 HisSerValAspProLysAsnThrIleTyrThrHisLeuThrThrGlnIleProAla 543
Qy 1699 ATCAAGGTAACTCTTGATACAACTCTAAGGTAAATTAAGGACCTGGTCATACAGGA 1758
Db 544 ValLysAlaAenSerLeuGlyThrAlaSerLysValValGlnGlyProGlyHisThrGly 563
Qy 1759 GGAACCTTGGTTTATTTTACAAAGTCAAGGGCGTTTGTAGAGATTACATGTAGAACTCT 1818
Db 564 GlyAspLeuIle-----AspPheLysAspHisPheLysIleThrCysGlnHisSerAen 581
Qy 1819 TCTACAACTTATACATTTAGACTTCGATACCGTACAAATGTGTGCGGAATATCTCT 1878
Db 582 PheGlnGlnSerTyrPheIleArgTyrAlaSerAenGlySerAlaAenThrArg 601
Qy 1879 CCTAATATCTCTTACAAATCAGGAGTAAATAGGAATACCACTCAACGACTCAACAAC 1938
Db 602 AlaValIleAenLeuSerIleProGlyValAlaGluLeu---GlyMetAlaLeuAenPro 620
Qy 1939 ACTTTTCTGTGACAAATTAATAATAATTAACAATACGAGATTTTGGGTATTTCCAATTT 1998
Db 621 ThrPheSerGlyThrAspTyrThrAsnLeuLysTyrLysAspPheGlnTyrLeuGluPhe 640
Qy 1999 CCAAGTACAGTAACATTAACCTTTTAAATCGAAACATACCATTTATATTAATTCGTCAG 2058
Db 641 SerAenGluValLysPheAlaProAenGlnAenIleSerLeuValPheAenArgSerAsp 660
Qy 2059 GTA---TCAATTCATTTTATCATATAAATTAATTAATTAATTAATTAATTAATTAAT 2115
Db 661 ValTyrThrAsnThrThrValIleuIleAspLysIleGluPheLeuProIleThrArgSer 680
Qy 2116 GTACCCCAAAATAGAGAAAAACAAAAATTAGAAATCTATCCAAACAAAAAATAATATCAT 2175
Db 681 IleArgGluAspArgGluLysGlnLysLeuGluThrValGlnGlnIleAenThrPhe 700
Qy 2176 TTCAAATCATACAAAAAATCTTTAATATATAGAGCCCAAACTATGATATGAT 2232
Db 701 TyrAlaAenProIleLysAenThrLeuGlnSerGluLeuThrAspTyrAspIleAsp 719

RESULT 9

US-09-756-526A-4
Sequence 4, Application US/09756526A
Patent No. US20020038005A1
GENERAL INFORMATION:
APPLICANT: Jana, Wojciechowska
APPLICANT: Evgeny, Lewitin
APPLICANT: Ludmila, Revina
APPLICANT: Igor, Zalunin
APPLICANT: Galina, Chesukhina
TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR.
FILE REFERENCE: S-30913A
CURRENT APPLICATION NUMBER: US/09/756,526A
PRIORITY FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: US 60/175,158
PRIOR FILING DATE: 2000-01-07

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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1109
; TYPE: PRN
; ORGANISM: Bacillus thuringiensis
US-09-756-526A-4

Alignment Scores:
Pred. No.: 1.4e-65 Length: 1109
Score: 901.00 Matches: 240
Percent Similarity: 49.29% Conservative: 106
Best Local Similarity: 34.19% Mismatches: 242
Query Match: 22.87% Indels: 114
DB: 3 Gaps: 27

US-10-782-570-1 (1-2235) x US-09-756-526A-4 (1-1109)
QY 199 AGTCTGATACAAATGCTGCAGTTAGTCAGGTACTATTGTATCGGTACTCTGTAGCC 258
DB 28 SerSerAepThrValAlaValSerAlaGlyLeValValValGlyThrIleLeuThr 47
QY 259 GGTATAGTGGGCTCACTTCTATATCCGACCGATAGGAATAAATAGGTGCTATATAATA 318
DB 48 -----AlaPheAlaSerPheValAsnPro-----GlyValValLeuIle 60
QY 319 TCTTTTGGTACCTTAATCACTGCTTTTGGCCCGGGGAGAACAGAC---AAACAGTA 375
DB 61 SerPheGlyThrLeuAlaProValLeuTrpProAepProGluGluAepProLysLysIle 80
QY 376 TGGACACAAATTTATAAATGGGAATTTTGTGTATACACCGTTTAAACAGAAAGCAT 435
DB 81 TrpSerGlnPheMetGlyHieGlyLeuAspLeuLeuAsnGlnThrIleSerThrAlaVal 100
QY 436 AAACAGCTAAAGTTACAACTTTAGACGATTTAGACAAATATTACAAAGCTATAATACA 495
DB 101 LysGluIleAlaLeuAlaHieLeuAsnGlyPheLysAepValLeuThrTyTrpGluArg 120
QY 496 GCATTAGATGTGAGAAATTTAAAGACTACAAAGCTCTCGGATTAACCACTATCA 555
DB 121 AlaPheAsnAepTrpLysArg-----AsnProSerAla 131
QY 556 GCATTACAAAGCTGCTTGAATTAAGATTTGAGATTTGCAATGATTTT 615
DB 132 -----AsnThrAlaArgLeuValSerGlnArgPheGluAsnAlaHiePheAsnPhe 148
QY 616 ATTCGAGAAATACCTGGTTTCAACTTAAAGCTTATAAAGCTTACTACTACTATTAT 675
DB 149 ValSerAsnMetProGlnLeuGlnLeuProThrTyTrpAepThrLeuLeuLeuSerCysTy 168
QY 676 GCGCAAGCTGCTAATTTTCAATTTAATTTATACAAAGTGTGTAATGGCTGATGAA 735
DB 169 ThrGluAlaAlaAsnLeuHieLeuAsnLeuLeuHieGlnGlyValGlnPheAlaAepGln 188
QY 736 TGGAAATGAGATATACATCTTCAAAATTCGAATTCGAATTCGAATTCAGATGACTAT 795
DB 189 TrpAsnAlaAepGlnProHieSerProMetLeuLysSerSerGlyThr-----Tyr 205
QY 796 TATAAATTTTAAAGAAATATACCTAAATATAGTAACTATTGCAAAATACCTATAGA 855
DB 206 TyrAepGluLeuLeuValTyIleGluLysTyIleAsnTyTrpThrLysThrTyHis 225
QY 856 GAAGACTTAAATAAATCTCGAAACGAACCTAATATAGATGGAGTATATTTAATGATTAT 915
DB 226 LysGlyLeuAsnHieLeuLysGluSerGluLysIleThrTrpAepAlaTyAsnThrTy 245
QY 916 CGAAGATATATGCTTACTGTTATGATCTACTATCGTCAATTTCTTTTATGATATA 975
DB 246 ArgArgGluMetThrLeuIleValLeuAspLeuValAlaThrPheProPheTyAspIle 265
QY 976 AAGAGATACAAAGATTCAATAGGAAGATAGTGGCATTAAACTGAACTTACAGAGAA 1035
DB 266 ArgArgPhePro-----ArgGlyValGluLeuLeuLeuThrArgGlu 279

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QY 1036 ATTTATACAACTGAAATAAATTTTGACCGTCTTACTTACCTTGAAATTCACCAATCTC 1095
DB 280 ValTyThrSer-----LeuAspHieLeuThrArgProGly--- 292
QY 1096 GCTATATGGAATATAATTTAACACGTTTCAGGGCTTAGATATTATTTTATAGTAA 1155
DB 293 -----LeuPheThrTrpLeuSerAep 299
QY 1156 CTTATATTTTATACAAAAATGAAACGTACGGGAATCGTTAGTTGGTATTGCGAATCGT 1215
DB 300 IleGluLeuTyThrGluSerValAlaGluGlyAspTyTrpLeuSerGlyIle----- 316
QY 1216 AATAGATCTACTTATGCTACGACAGGAACCTGAATTT-----ATATATGGA 1260
DB 317 ---ArgGluSerLysTyTrpTyThrGlyAsnGlnPhePheThrMetLysAsnIleTyGly 335
QY 1261 GAAAGACAGGTCCACCCACCAACAAA-----ACTTTAATACCAATTT 1302
DB 336 Asn-----ThrAsnArgLeuSerLysGlnLeuIleThrLeuLeuProGly 350
QY 1303 GAATCTCTATAAAGTTTCAATTGTAACTGATAGACAACTCTCTACTTCCCTTTTCTCT 1362
DB 351 Glu---PheMetThrHieLeuSerIleAsnArgProPheGlnThrIleAlaGlyLeuAsn 369
QY 1363 AACATATCTTTCAATAATCAAAATTTGAATTTTAAATTAATTAATCACTAGTAATAAA 1422
DB 370 LysLeuTySerLeuIleGlnLysIle-----ValPheThrThrPheLysAsnAep 386
QY 1423 TTAACATATTTCAGCTGGGGGAATTTATCTAATGAT-----AAAAAACCACTGAT 1473
DB 387 AsnGluTyGlnLysAsnPheAsnValAsnAsnGlnAsnGluProGlnGluThrAsn 406
QY 1474 TTTCAATTTCTGTAAAAAAGACTGTAAACCAATTTAATTAATCCAAATTTGTTACCAAGC 1533
DB 407 Tyr-----ProAsnAepTyTrpGlyGly 413
QY 1534 TATAATAGT-----TATAGTCATATTTTATCCAGTTTCTTTTATTAATTTATTCCTAT 1587
DB 414 SerAsnSerGlnLysPheLysHieAsnLeuSerHiePheProLeuIleHieHieLysLeu 433
QY 1588 AAAATTCGATTAGCGCTAATATATATATATACAGGTGCATTAGGTACGACACAGTAGT 1647
DB 434 GluPheAlaGluTyPheHieSerIlePhe-----AlaLeuGlyTyTrpThrHieAsnSer 451
QY 1648 GTTAATAGAAATATGCAATATCAGATATAAATTAATCAATATGATCCACGCAATCAAAAGT 1707
DB 452 ValAsnSerGlnAsnLeuIleSerGluSerValSerThrGlnIleProLeuValLysAla 471
QY 1708 AACAGTCTTGATCAAACTCTAAGTTAATTTGAAGGACCTCGTCAATACAGAGGAACTTG 1767
DB 472 TyrGluVal---ThrAsnAsnSerValIleArgGlyProGlyPheThrGlyGlyAspLeu 490
QY 1768 GTTTATTACAAAGTCAAGGGCTTAGAGATTACATGTAGAACTCTCTAATTTCTACACAA 1827
DB 491 IleLeuLeuArgAep-----LysCysSerIleLysCysLysAla---SerSerLeuLys 507
QY 1828 TCTTATTACATAGCTTCGATACGCTACAAATGGTGTGCTGGAATACTCTTCTCTAATATA 1887
DB 508 LysTyTrpAlaIleSerLeuPheTyAlaAlaAsnAlaIleAlaValSerIleAspVal 527
QY 1888 TCTCTTACATACAGAGGTAATAGGAATACCACTCAAGCTCAACACACACTTTTCT 1947
DB 528 GlyAspSerGlyAlaGlyValLeu-----LeuGlnProThrPheSer 541
QY 1948 GGTACAAATTTATATAT-----TTACAATACGAGATTTTGGTATTTC 1992
DB 542 ArgLysGlyAsnAsnAsnPheThrIleGlnAspLeuAsnTyTrpLysAepPheGlnTyHis 561
QY 1993 CAATTTTCCAGTAGTAAACATTTTAAATCGAAACACATCACTATTTATTTTAAATCGT 2052
DB 562 ThrLeuLeuValAspIleGluLeuProGluSerGluGluIleHieHieLysLeuArg 581

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QY	2053	GCAGAT-----GTATCAAAATTCAAATTTTAATCATTTGATATAAAATTCGATTTATACCAATT	2106
Db	582	GLUaSPaSPtyrGluGluGluValIleLeuLeuIleAspLysLeuGluPheLysProIle	601
QY	2107	ACTTCTCTGTATCGCCAAATATAGAGAAACAAAATTTAGAACTATCCAAACAAAAATA	2166
Db	602	AspGluasnTyr-----ThrAsnGluMetAsnLeuGluLysAlaLysAlaVal	618
QY	2167	AATACATATTTTTCACAAATCATACAAAAATACTTTTAAATATAGAGCCACAAACTATGAT	2226
Db	619	AsnValLeuPheIleAsnAlaThr---AsnAlaLeuLysMetAspValThrAspTyrHis	637
QY	2227	ATTGAT 2232	
Db	638	IleAsp 639	
RESULT 10			
US-10-345-020-4			
; Sequence 4, Application US/10345020			
; Publication No. US20030150018A1			
; GENERAL INFORMATION:			
; APPLICANT: Jana, Wojciechowska			
; APPLICANT: Evgeny, Lewitin			
; APPLICANT: Ludmila, Revina			
; APPLICANT: Igor, Zalunin			
; TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR			
; FILE REFERENCE: S-309138			
; CURRENT APPLICATION NUMBER: US/10/345,020			
; CURRENT FILING DATE: 2003-01-15			
; PRIOR APPLICATION NUMBER: US 60/175,158			
; PRIOR FILING DATE: 2000-01-07			
; NUMBER OF SEQ ID NOS: 5			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 4			
; LENGTH: 1109			
; TYPE: PRT			
; ORGANISM: Bacillus thuringiensis			
US-10-345-020-4			
Alignment Scores:			
Pred. No.: 1.4e-65 Length: 1109			
Score: 901.00 Matches: 240			
Percent Similarity: 49.29% Conservative: 106			
Best Local Similarity: 34.19% Mismatches: 242			
Query Match: 22.87% Indels: 114			
DB: 4 Gaps: 27			
US-10-782-570-1 (1-2235) x US-10-345-020-4 (1-1109)			
QY	199	AGTGCTCATCAAAATTCGTGCGAGTACTATTGTATCGGTACTCTGTTAGACC	258
Db	28	SerSerAspThrValAlaValValSerAlaGlyLeuValValGlyThrIleLeuThr	47
QY	259	GGTATAGGTGGGCTCCTCTATATCGGACCCGATAGGAATAATAGTGTCTATAATAATA	318
Db	48	-----AlaPheAlaSerPheValAsnPro-----GlyValValLeuIle	60
QY	319	TCCTTTGGTACCTTAATCCTGCTTTTGGCCCGGGAGAACAGAC---AAACAGTA	375
Db	61	SerPheGlyThrLeuAlaProValLeuTyrProAspProGluGluAspProLysLysIle	80
QY	376	TGGACAAATTTATTAATGGGAGAAATTTTCTGTATACACCGTTTAAACAGAAAGCATA	435
Db	81	TrpSerGlnPheMetLysHisGlyGluAspLeuAsnGlnThrIleSerThrAlaVal	100
QY	436	AAACAGCTAAAGTTACAAACTTTTAGAAGGATTTAGACAAATATTAACAAAGCTATAATACA	495
Db	101	LysGluIleAlaLeuAlaHisLeuAsnGlyPheLysAspValLeuThrTyrTyrGluArg	120
QY	496	GCATTAGATGATCGAGAAATTTAAAGACTACAAGCTCTCGGATTACCAACCATATCA	555
Db	121	AlaPheAsnAspTyrLysArg-----AsnProSerAla	131

Qy 1588 AAAATTGGATTAGCGCTAAATATAATTAATATACAGGTGCATTGCAATCCAGCACAACACTAGT 1647
:
Dd GluPheAlaGlutyrPheHisSerIlePhe-----AlaLeuGliYrThrHisAsnSer 451
:: :: ::
Qy 1648 GTTTATAGAATAATGCNAATCATAGATAAATAATTAACAATGATCCCAGCAATCAAAGGT 1707
|||||
Dd ValAsnSerGlnAsnLeuIleSerGluSerValSerThrGlnIleProLeuValLysAla 471
||| | : : : : :
Qy 1708 AACAGTCCTTGATCAAAAATCTTAAGGTGAATGGAAGGACCCTGGTCATACAGGAGGAAAACTTG 1767
:: |||||
Dd TyrGluVal---ThrasnaAsnSerValileargGlyProgdyPhethrGlyGlyAspLeu 490
||| | : : : : :
Qy 1768 GTTTTATTATCACAAAGTCGAAGGCCGTTTAGAGAGATTACATGTAGAACCTCCTAATTTCTACACAA 1827
: |||||
Dd IleGluLeuArgAsp-----LysCysSerIleLysCysLysala---SerSerLeuLys 507
||| | : : : : :
Qy 1828 TCTTTATTACATTAGACTTCGNATCGCTCAAAATGGTGCTCGAANAATCTCTTCTCTAATATA 1887
||| | : : : : :
Dd LystyrAlatIleSerLeuPheTyAlaAlaAsnAlaIleAlaValSerIleAspVal 527
||| | : : : : :
Qy 1888 TCTCTTCAAAATACCAAGGAGTAATAGGAATACCACTCAAGACTCAACAACACTTTTCT 1947
:: |||||
Dd GlyaspSerglyAlaGlyValLeu-----LeuGlnProThrPheSer 541
||| | : : : : :
Qy 1948 GGTCAAAATATATAAAT- - - - -TTACAATACGGAGATTTTGGGTATTTCT 1992
||| | : : : : :
Dd ArglysGlyAsnAsnAsnPheThrIleGlnAspLeuAsnTYrLYSAspPheGlnTYRHis 561
||| | : : : : :
Qy 1993 CAATTTCCAAGTACAGTAAACATACCTTTTAAATCGAAACATACCATTTATTTAATCGT 2052
:||| : : : : :
Dd ThrLeuLeuValAspIIeGluLeuProGLUSerGluGluIleHISleHisLeuLysArg 581
||| | : : : : :
Qy 2053 GCAGT-----GTATCAAAATTCAAATTTTAAATCATGTATAAAATTTGAATTTATACCAATT 2106
||| | : : : : :
Dd GluaspaspyrGluGluGlyValIleuLeuleaspLysLeuGluPheLysProIle 601
||| | : : : : :
Qy 2107 ACTTCCTCTGTACGCCAAAATAGAGAAAAACAAAATATAGAAACTATCCAAAACAAAATA 2166
:: |||||
Dd AspGluAsnTYR-----ThraSnGluMetAsnLeuGluLysAlaLysAlaVal 618
||| | : : : : :
Qy 2167 AATACATTTTTCACAAATCATACAAAAAATCTTTAAATATAGAGCCACAAACTATGAT 2226
||| | : : : : :
Dd AsnValLeuPheIleAsnAlaThr---asnAlaleuLysMetaspValThrAspyrtyrHis 637
||| | : : : : :
Qy 2227 ATTGAT 2232
||| | : : : : :
Dd IleaSp 639
||| | : : : : :

RESULT 11
US-10-342-821-4 ; Sequence 4, Application US/10342821
; Publication No. US20030154510A1
; GENERAL INFORMATION:
; APPLICANT: Jana, Wojciechowska
; APPLICANT: Evgeniy, Lewitin
; APPLICANT: Ludmila, Revina
; APPLICANT: Igor, Zaludin
; APPLICANT: Galina, Chestukhina
; TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR
; FILE REFERENCE: S-30913C
; CURRENT APPLICATION NUMBER: US/10/342,821
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/175,158
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1109
; TYPE: PRF
; ORGANISM: Bacillus thuringiensis
US-10-342-821-4
Alignment Scores:


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QY 1156 CTTATATTTTATACAAAAAATGAACGATGACGGGAATCGTTAGTTGGTATTCGGAATCGT 1215
Db 1156 CTTATATTTTATACAAAAAATGAACGATGACGGGAATCGTTAGTTGGTATTCGGAATCGT 1215
QY 300 ILeGluLeuTyThrGluSerValAlaGluGlyAspTyrLeuSerGlyLe-----ATATATCGA 1260
Db 300 ILeGluLeuTyThrGluSerValAlaGluGlyAspTyrLeuSerGlyLe-----ATATATCGA 1260
QY 1216 AATAGATCTATCTGCTACGACGAGAACTGAAAT-----ATATATCGA 1260
Db 1216 AATAGATCTATCTGCTACGACGAGAACTGAAAT-----ATATATCGA 1260
QY 317 ---ArgGluSerLysTyThrGlyAsnGlnPheThrMetLysAsnIleTyGly 335
Db 317 ---ArgGluSerLysTyThrGlyAsnGlnPheThrMetLysAsnIleTyGly 335
QY 1261 GAAAGAACAGGTCACCCACACAA-----ACTTTATACCAATTT 1302
Db 1261 GAAAGAACAGGTCACCCACACAA-----ACTTTATACCAATTT 1302
QY 336 Asn-----ThrAsnArgLeuSerLysGlnLeuIleThrLeuLeuProGly 350
Db 336 Asn-----ThrAsnArgLeuSerLysGlnLeuIleThrLeuLeuProGly 350
QY 1303 GAATCTTATAAAGTTTCAATTTGATGATGACGACAAAGTAATCTCTCTCTCTCTCTCTCTCT 1362
Db 1303 GAATCTTATAAAGTTTCAATTTGATGATGACGACAAAGTAATCTCTCTCTCTCTCTCTCTCT 1362
QY 351 Glu---PheMetThrHisLeuSerIleAsnArgProPheGlnThrIleAlaGlyLeAsn 369
Db 351 Glu---PheMetThrHisLeuSerIleAsnArgProPheGlnThrIleAlaGlyLeAsn 369
QY 1363 AACATATCTTACATTAATCAATTCGAATTTTATTTAATAATTAATTCACCTAGTAATAA 1422
Db 1363 AACATATCTTACATTAATCAATTCGAATTTTATTTAATAATTAATTCACCTAGTAATAA 1422
QY 370 LysLeuTySerLeuIleGlnIle-----ValPheThrThrPheLysAsnAsp 386
Db 370 LysLeuTySerLeuIleGlnIle-----ValPheThrThrPheLysAsnAsp 386
QY 1423 TTAACATATTCAGCTGGGGGAATTTATCTAATGAT-----AAAAAACCACTGAT 1473
Db 1423 TTAACATATTCAGCTGGGGGAATTTATCTAATGAT-----AAAAAACCACTGAT 1473
QY 387 AsnGluTyGlnLysAsnPheAsnValAsnAsnGlnAsnGluProGlnGluThrAsn 406
Db 387 AsnGluTyGlnLysAsnPheAsnValAsnAsnGlnAsnGluProGlnGluThrAsn 406
QY 1474 TTTCAATTTCTGTAAAAAAAGACTGTAAACCAATTTATTAATCCAAATTTGTTTACCAAGC 1533
Db 1474 TTTCAATTTCTGTAAAAAAAGACTGTAAACCAATTTATTAATCCAAATTTGTTTACCAAGC 1533
QY 407 Tyr-----ProAsnAspTyGlyGly 413
Db 407 Tyr-----ProAsnAspTyGlyGly 413
QY 1534 TATAATAGT-----TATAGTCATATTTTATCCAGATTTCTTTTATTAATTTATTCCTAT 1587
Db 1534 TATAATAGT-----TATAGTCATATTTTATCCAGATTTCTTTTATTAATTTATTCCTAT 1587
QY 414 SerAsnSerGlnLysPheLysHisAsnLeuSerHisPheProLeuIleIleHisLysLeu 433
Db 414 SerAsnSerGlnLysPheLysHisAsnLeuSerHisPheProLeuIleIleHisLysLeu 433
QY 1588 AAAATTCGATAGCTGCTAAATATATATATATATATATATATATATATATATATATATATAT 1647
Db 1588 AAAATTCGATAGCTGCTAAATATATATATATATATATATATATATATATATATATATATAT 1647
QY 434 GluPheAlaGluTyPheHisSerIlePhe-----AlaLeuGlyTyPheHisAsnSer 451
Db 434 GluPheAlaGluTyPheHisSerIlePhe-----AlaLeuGlyTyPheHisAsnSer 451
QY 1648 GTTATAGAAATATGCAATATCAGATATAATTAATTAATGATCCAGCAATCAAGGT 1707
Db 1648 GTTATAGAAATATGCAATATCAGATATAATTAATTAATGATCCAGCAATCAAGGT 1707
QY 452 ValAsnSerGlnAsnLeuIleSerGluSerValSerThrGlnIleProLeuValIleAla 471
Db 452 ValAsnSerGlnAsnLeuIleSerGluSerValSerThrGlnIleProLeuValIleAla 471
QY 1708 AACAGCTCTTATACAACTTAAGTAAATTAAGAGCTGCTGTCATACAGGAGGAACTTG 1767
Db 1708 AACAGCTCTTATACAACTTAAGTAAATTAAGAGCTGCTGTCATACAGGAGGAACTTG 1767
QY 472 TyrGluVal---ThrAsnAsnSerValIleArgGlyProGlyPheThrGlyAspLeu 490
Db 472 TyrGluVal---ThrAsnAsnSerValIleArgGlyProGlyPheThrGlyAspLeu 490
QY 1768 GTTATATTTACAAAGTCAGGGGCTTACAGATATACATGATGATGATGATGATGATGATGATGAT 1827
Db 1768 GTTATATTTACAAAGTCAGGGGCTTACAGATATACATGATGATGATGATGATGATGATGATGAT 1827
QY 491 IleGluLeuArgAsp-----LysCysSerIleLysCysLysAla---SerSerLeuLys 507
Db 491 IleGluLeuArgAsp-----LysCysSerIleLysCysLysAla---SerSerLeuLys 507
QY 1828 TCTTATACATTTAGACTTCGATACGCTACAAATGCTGCTGGAAATATCTCTCTCTTAATATA 1887
Db 1828 TCTTATACATTTAGACTTCGATACGCTACAAATGCTGCTGGAAATATCTCTCTCTTAATATA 1887
QY 508 LysTyraIleSerLeuPheTyraIleAlaAsnAsnAlaIleAlaValSerIleAspVal 527
Db 508 LysTyraIleSerLeuPheTyraIleAlaAsnAsnAlaIleAlaValSerIleAspVal 527
QY 1888 TCTCTTACATACACGAGGATATAGGAATACCACTCAACGACTCAACACACTTTTCT 1947
Db 1888 TCTCTTACATACACGAGGATATAGGAATACCACTCAACGACTCAACACACTTTTCT 1947
QY 528 GlyAspSerGlyAlaGlyValLeu-----LeuGlnProThrPheSer 541
Db 528 GlyAspSerGlyAlaGlyValLeu-----LeuGlnProThrPheSer 541
QY 1948 GGTACAAATTTAATAAT-----TTACAATACGAGATTTTGGGTATTC 1992
Db 1948 GGTACAAATTTAATAAT-----TTACAATACGAGATTTTGGGTATTC 1992
QY 542 ArgLysGlyAsnAsnAsnPheThrIleGlnAspLeuAsnTyLysAspPheGlnTyHis 561
Db 542 ArgLysGlyAsnAsnAsnPheThrIleGlnAspLeuAsnTyLysAspPheGlnTyHis 561
QY 1993 CAATTTCCAAGTACAGTAACTTACTTTAAATCGAAACATACCACTTATATTTAATCGT 2052
Db 1993 CAATTTCCAAGTACAGTAACTTACTTTAAATCGAAACATACCACTTATATTTAATCGT 2052
QY 562 ThrLeuLeuValAspIleGluLeuProGluSerGluGluIleHisIleHisLeuLysArg 581
Db 562 ThrLeuLeuValAspIleGluLeuProGluSerGluGluIleHisIleHisLeuLysArg 581
QY 2053 GCAGAT-----GTATCAAAATTTAATTTAATGATGATGATGATGATGATGATGATGATGAT 2106
Db 2053 GCAGAT-----GTATCAAAATTTAATTTAATGATGATGATGATGATGATGATGATGATGAT 2106
QY 582 GluAspAspTyGluGluGlyValIleLeuLeuIleAspLysLeuGluPheLysProIle 601
Db 582 GluAspAspTyGluGluGlyValIleLeuLeuIleAspLysLeuGluPheLysProIle 601
QY 2107 ACTTCTCTGTACGCCCAAAATAGAGAAAACAAAATTTAGAACTATCTCAACCAAAATA 2166
Db 2107 ACTTCTCTGTACGCCCAAAATAGAGAAAACAAAATTTAGAACTATCTCAACCAAAATA 2166
QY 602 AspGluAsnTy-----ThrAsnGluMetAsnLeuGluLysAlaLysLysAlaVal 618
Db 602 AspGluAsnTy-----ThrAsnGluMetAsnLeuGluLysAlaLysLysAlaVal 618
QY 2167 AATACATTTTTCACAAATCATACAAAAAATACTTTTAAATATATAGAGCCCAAACTATGAT 2226
Db 2167 AATACATTTTTCACAAATCATACAAAAAATACTTTTAAATATATAGAGCCCAAACTATGAT 2226
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Db 619 AsnValLeuPheIleAsnAlaThr---AsnAlaLeuLysMetAspValThrAspTyrHis 637
QY 2227 ATTGAT 2232
Db 638 IleAsp 639
RESULT 12
US-10-782-141-17
; Sequence 17, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-17
Alignment Scores:
Pred. No.: 2,69e-65 Length: 675
Score: 897.00 Matches: 251
Percent Similarity: 47.96% Conservative: 114
Best Local Similarity: 32.98% Mismatches: 268
Query Match: 22.77% Indels: 128
DB: 4 Gaps: 32
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US-10-782-570-1 (1-2235) x US-10-782-141-17 (1-675)
QY 13 AATAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 72
Db 6 AsnLysAsnGluTyGluIlePheAsnAlaProSerAsnGlyPheSerLysSerAsnAsn 25
QY 73 ATTGATCTTCTAGATACCTTACACAAATTAATCAAAATCAACCAATCAACCAATCAACCAAT 132
Db 26 -----TyrSerArgTyrProLeuAlaAsnLysProAsnGlnProLeuLysAsnThrAsn 43
QY 133 TACAAGAGTCGCTCAATATGTCACAGGGAATACACAAATATGATGATGATGATGATGATGATGAT 192
Db 44 TyrllysAspTyrLeuAsnValCysGlnAspAsnGlnGlnTyrglyAsnAsnAlaGlyAsn 63
QY 193 TTTGCTAGTCTGATACAAATTCGTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGT 252
Db 64 PheAlaSerSerGluThrIleValGlyValSerAlaGlyIleIleValValGlyThrMet 83
QY 253 TTAGCCGGTATAGTGGGCTCCTCTATATATCCGACCGATAGGAAATATAGTGTCTCTATA 312
Db 84 LeuGly-----AlaPheAlaAlaPro-----ValLeuAlaAlaGly 95
QY 313 ATATATCTTTTGGTACCTTAATCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 372
Db 96 IleIleSerPheGlyThrLeuLeuProIlePheTrp-----GlnGlySerAspProAlaAsn 114
QY 373 GTATGGACACAAATTTATTAATAATGGGAAATATTTTGTGTATACACCGTTAACAGAA--- 429
Db 115 ValTrpGlnAspLeuLeuAsnIleGly-----GlyArgProIleGlnGluIle 130
QY 430 -----ACGATAAAACAGCTAAAGTTACAAACTTTAGAGAGGATTTAGACAAATATATACAA 483
Db 131 AspLysAsnIleIleAsnValIleuThrSerIleValThrProIleLysAsnGlnLeuAsp 150
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QY	484	AGCTATAATACACGCAATTAGATGATTTGGAGAAAAATTAAAGAGACTACAAGCTCCCTGGATTA	543
DB	151	LyStyGInGluPheAeSPlStpGluProAlaArg-----	163
QY	544	CCACCATCATCAGCAATTACACACAGCTCCCTTGACTCTTAAATACGATTTGAGAAATGTT	603
DB	164	-----ThrHisAlaAsnAlaLysAlaValHisAeSPlLeuPheThrThrLeuGluProIle	181
QY	604	CACAAAT-----GATTTATTTCGAGAAATACCTGTTTCCCACTTGAACCTATATAA	654
DB	182	IleAeSPlAeSPlLeuAeSPlMetLeuLysAsnAsnAlaSerTyArgIleProThr-----	199
QY	655	AGCGTATTACTACTATTATTATCGGCAAGCTGCTAATTTTCATTTAAATTTATTAACAACA	714
DB	200	-----LeuProAlaTyAlaGlnIleAlaThrTrpHisLeuAsnLeuLysHis	216
QY	715	GGTGTGAATTTGGCTGATGAATGCAATGCAGATATACATCTTCACAAATGAACCTAAT	774
DB	217	AlaAlaThrTyTyArgAsnIleTrp-----LeuGlnAsnGlnGlyIleAsnProSer	233
QY	775	GCTGGAACATCAGATGACTATTATAA---CTTTAAAGAAAAATATACCTAAATATAGT	831
DB	234	ThrPheAsnSerSerAsnTyTyGlnGlyTyLeuLysArgLysIleGlnGluTyThr	253
QY	832	AACATTATGTCAAATACCTATAGAGAAGGACTAAATAAATTAACCTGCAACGACCTAATATG	891
DB	254	AspTyCySileGlnThrTyArgAsnAlaGlyLeuThrMetIleArgThrAsnThrAsnAla	273
QY	892	AGATGGAGTATATTTAATGATATTCGAAGATATATGACTATTACTGTATTAGATACTATC	951
DB	274	ThrTrpAsnMetTyAsnThrTyArgLeuGluMetThrLeuThrValLeuAspLeuIle	293
QY	952	GCTCAATTTCTTTTATGATATAAGAGATACAAAGATTCAATAGGAAGAATAGGTGGC	1011
DB	294	AlaIlePheProAsnTyAspProGluLysTyProIle-----Gly	307
QY	1012	ATTAAGACTGAACCTTACAAGAGAAATTTATACAACTGAAATATAATTTTGACCGCTTACT	1071
DB	308	ValLysSerGluLeuIleArgGluValTy---ThrAsnValAsnSerAspThrPheArg	326
QY	1072	TACCTTGAAATTCACCCCATCTCGCTATATATGGAATATATTAATTAACACGTTTCAGGGCTT	1131
DB	327	-----ThrIleThrGluLeuGluAsnGlyLeuThrArgAsnPro---	339
QY	1132	AGATTATTTTCATTTTATGATGAACCTATATTTTATACAAAAAT-----	1176
DB	340	ThrLeuPheThrTrpIleAsnGlnGlyArgPheTyThrArgAsnSerArgAspIleLeu	359
QY	1177	GAACAGTGAC-----GGGAATCGTTTGTATGCTATTTGCGAATCGTAAAT	1218
DB	360	AspProTyAspIlePheSerPheThrGlyAsnGlnMetAla-----	373
QY	1219	AGATCTACTTATGCTACACAGGAACCTGAATATATATATATGAGAGAAAGACAGGT---	1272
DB	374	---PheThrHisThrAsnAspAspArgAsnIleIleTrpGlyAlaValHisGlyAsnIle	392
QY	1273	--CCACCCACAACAAACCTTTAATACCAATTCGAATCCTAT-----AAAGTT	1317
DB	393	IleSerGlnAspThrSerLysValPheProPheTyArgAsnLysProIleAspLysVal	412
QY	1318	TCAATTTGAATGATAGACAAAGTAACCTACTTCCCTCTTTCCTAACATATATCTTACA	1377
DB	413	GluIleValArgHisArgGlu-----TyrSerAsp	422
QY	1378	ATTAATCAAAATGAACCTTTATTTAAATAATTCACCTAGTAAATTAATTAACATATTCAGCT	1437
DB	423	IleIleTyGluMetIlePhePheSerAsnSer---SerGluValPheArgTySerSer	441
QY	1438	GGGGGGGAATTTATCTAATGATATAAAAAACAACGATTTTCAATTTCTGTAAAAAAGAC	1497
DB	442	AsnSerThrIleGluAsnAsnTyLysArgThrAspSerTyMetIleProLysGlnThr	461

[illegible]


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QY 1915 ATACCACCTCAACGACTCAACAAACACTTTTCTGTCACAAATTATAAT-----AATTTA 1968
Db      :::: |||| :::: |||| |||| |||| |||| |||| |||| |||| |||| ||||
582 IleserValGlu---LeuProSerThrThrSerArgGlnAsnProAsnAlaThrAspLeu 600
QY 1969 CAATACGAGATTGTTGGGTATTTCCTCAATTTCCAAAGTACAGTA----- 2010
Db      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
601 ThrTyAlaAspPheGlyTy-ValThrPheProArgThrValProAsnLysThrPheGlu 620
QY 2011 -----ACATACCTTTAAATCGAAACATACACNTTATATTATTAATCGTCGAGATGA 2061
Db      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
621 GlyGluAspThrLeuLeuMetThr-----LeuTyGlyThrProAsnHis 635
QY 2062 TCAATTCATTTTAAATCATGATAAAATGAAATTTATACCAATTTACTCTCTGTACGC 2121
Db      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
636 SerTyAsnIle---TyriLeAspLysIleGluPheIleProIleThrGlnSerValLeu 654
QY 2122 CAAATAGAGAAAAACAAAAATTAGAACTATCCAAACAAAAATAATATACATTTTTCACA 2181
Db      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
655 AspTyThrGluLysGlnAsnIleGluLysThrGlnLysIleValAsnAspLeuPheVal 674
QY 2182 AAT 2184
Db      ||||
675 Asn 675

RESULT 14
US-10-782-570-14
; Sequence 14, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Haigies, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-14

Alignment Scores:
Pred. No.: 2,69e-65 Length: 675
Score: 897.00 Matches: 251
Percent Similarity: 47.96% Conservative: 114
Best Local Similarity: 32.98% Mismatches: 268
Query Match: 22.77% Indels: 128
DB: 4 Gaps: 32

US-10-782-570-1 (1-2235) x US-10-782-570-14 (1-675)
QY 13 AATAATAATGAATGAGATTATCGATTCAAGAAATTTATCTTCTCTTCAACAGAAAT 72
Db      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
6 AsnLysAsnGluTyGluIlePheAsnAlaProSerAsnGlyPheSerLysSerAsnAsn 25
QY 73 ATTGATCAATCTAGATACCTTTACACAAATTAATCCAAATCAACCATTAACAAAACACAAAT 132
Db      :::: |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
26 -----TySerArgTy-ProLeuAlaAsnLysProAsnGlnProLeuLysAsnThrAsn 43
QY 133 TACAAGAGTGGCTCAATATGTCACGGGAATACAGAAATATGATGATTAATTTTCGAGACA 192
Db      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
44 TyriLysAspTrpLeuAsnValCysGlnAspAsnGlnGlnTyriGlyAsnAsnAlaGlyAsn 63
QY 193 TTTGCTAGTGTGATACAAATGCTGCTAGTGTAGTGCAGGTACTATTGTTATCCGGTACTCTG 252
Db      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||

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Db 64 PheAlaSerSerGluThrIleValGlyValSerAlaGlyIleIleValValGlyThrMet 83
QY 253 TTAGCCCGTATAGTGGCTCCTCTTATATCCGAGCGATAGGAATAATAAGTGGCTATA 312
Db      :::: |||| :::: |||| |||| |||| |||| |||| |||| |||| ||||
84 LeuGly-----AlaPheAlaAlaPro-----ValLeuAlaAlaGly 95
QY 313 ATATATCTTTTGTGTACCTTAATCAGCTGCTTTTGGCCCGCGGAGAACAGACAAAACA 372
Db      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
96 IleIleSerPheGlyThrLeuLeuProIlePheTrp---GlnGlySerAspProAlaAsn 114
QY 373 GTATGGACACAAATTTATTAATAATGGGAGAAATTTTGTGTATACACCGTTTAACAGAA--- 429
Db      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
115 ValTrpGlnAspLeuLeuAsnIleGly-----GlyArgProIleGlnGluIle 130
QY 430 -----AGCATAAACAGCTTAAGTTTCAAACTTTAGAGAGATTTAGACAAATATTACA 483
Db      :::: |||| :::: |||| |||| |||| |||| |||| |||| |||| ||||
131 AspLysAsnIleIleAsnValLeuThrSerIleValThrProIleLysAsnGlnLeuAsp 150
QY 484 AGCTATAATACAGCATTTAGATGATTGGAGAAAATTTAAAAAGACTACAAGCTCTCGGATTA 543
Db      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
151 LysTyThrGlnGluPhePheAspLysTrpLupProAlaArg----- 163
QY 544 CCACCATCATCAGCATTTACAAACAGCTGCCCTTGACTCTTAAATAACGATTTGAGAATGTT 603
Db      :::: |||| :::: |||| |||| |||| |||| |||| |||| |||| ||||
164 -----ThrHisAlaAsnAlaLysAlaValHisAspLeuPheThrThrLeuGluProIle 181
QY 604 CACAAAT-----GATTTTATTCGAGAAATACCTCGTTTCCAACTTGAACATTATAA 654
Db      :::: |||| :::: |||| |||| |||| |||| |||| |||| |||| ||||
182 IleAspLysAspLeuAspMetLeuLysAsnAsnAlaSerTyArgIleProThr----- 199
QY 655 ACGCTATTACTACTATTATGCGCAGCTGCTAAATTTTCATTTTAAATTTTATTACAACA 714
Db      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
200 -----LeuProAlaTyAlaGlnIleAlaThrTrpHisLeuAsnLeuLeuHis 216
QY 715 GGTGCTGAATTTGGCTGATGAATGCAATGCAGATATACATCTTCACAAAATGAACCTAAT 774
Db      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
217 AlaAlaThrTyThrAsnIleTrp-----LeuGlnAsnGlnGlyIleAsnProSer 233
QY 775 GCTGGAACATCAGATGACTATTATAAA---CTTTTAAAGAAATATACCTTAATATAGT 831
Db      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
234 ThrPheAsnSerSerAsnTyTyThrGlnGlyTyThrLysArgLysIleGlnGluTyThr 253
QY 832 AACTATTGTCAAATACCTATAGAGAGGACTAAATAAACTTCGAAACGAACTAAATATG 891
Db      :::: |||| :::: |||| |||| |||| |||| |||| |||| |||| ||||
254 AspTyThrCysIleGlnThrTyAsnAlaGlyLeuThrMetIleArgThrAsnThrAsnAla 273
QY 892 AGATGGAGTATATTTAATGATATCGAAGATATATGACTATTACTGTATTAGATACATC 951
Db      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
274 ThrTrpAsnMetTyThrAsnThrTyArgLeuGluMetThrLeuThrValLeuAspLeuIle 293
QY 952 GCTCAATTTTCTTTTATGATATAAGAGATACAAAGATTCATATGAGAAATAGGTGGC 1011
Db      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
294 AlaIlePheProAsnTyAspProGluLysTyProIle-----Gly 307
QY 1012 ATTAABAACTCACTTACACAGAAATTTATACAACTGAATAATTTTGGACCGCTTACT 1071
Db      :::: |||| :::: |||| |||| |||| |||| |||| |||| |||| ||||
308 ValLysSerGluLeuIleArgGluValTy---ThrAsnValAsnSerAspThrPheArg 326
QY 1072 TACCTTGAATTTCAACCAATCTCGCTATATGGAATATATATTTAAACACGTTTCAGGGCTT 1131
Db      :::: |||| :::: |||| |||| |||| |||| |||| |||| |||| ||||
327 -----ThrIleThrGluLeuGluAsnGlyLeuThrArgAsnPro--- 339
QY 1132 AGATTATTTTCACTTTTAGATGAACCTTATATTTTATACAAAAAT----- 1176
Db      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
340 ThrLeuPheThrTrpIleAsnGlnGlyArgPheTyThrArgAsnSerArgAspIleLeu 359
QY 1177 GAAACGTAC-----GGGAATCGTTTGTGTATTTGCTATTTGCGAATCGTAAT 1218
Db      :::: |||| :::: |||| |||| |||| |||| |||| |||| |||| ||||
360 AspProTyThrAspIlePheSerPheThrGlyAsnGlnMetAla----- 373
QY 1219 AGATCTACTTACTGTACGACAGAACTGAAATTTATATATATGAGAAAGAACAGGT- 1272
Db      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
374 ---PheThrHisThrAsnAspAspArgAsnIleIleTrpGlyAlaValHisGlyAsnIle 392

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Db      182 IleAspLysAspLeuAspMetLeuLysAsnAsnAlaSerTyrArgIleProThr----- 199
Qy      655 AGGCTATTACTACCTATTATGCGCAAGCTGCTAAATTTTCATTAAATTTATTACACAA 714
Db      200 -----LeuProAlaTyrAlaGlnIleAlaThrTrpHisLeuAsnLeuLeuLysHis 216
Qy      715 GGTGCTGAATGGCTGATGAATGGAATGCAGATATACATCTCTTCCAAATTTGAACCTAAT 774
Db      217 AlaAlaThrTyrTyrAsnIleTrp-----LeuGlnAsnGlnGlyIleAsnProSer 233
Qy      775 GCTGGAACATCAGATGACTATTATATAA---CTTTTAAAGAAAATATACCTTAAATATAGT 831
Db      234 ThrPheAsnSerSerAsnTyrTyrGlnGlyTyrLeuLysArgLysIleGlnGluTyrThr 253
Qy      832 AACTATTGTGCAAACTACCTATAGAGAGCACTAAATAAATCTCGAAACGACCTAATATG 891
Db      254 AspTyrCysIleGlnThrTyrAsnAlaGlyLeuThrMetIleArgThrAsnThrAsnAla 273
Qy      892 AGATGGAGTATATTTAATGATTATCGAAGATATATGACTATTACTGTGTTAGACTATC 951
Db      274 ThrTrpAsnMetTyrAsnThrTyrArgLeuGluMetThrLeuThrValLeuAspLeuLe 293
Qy      952 GCTCAATTTCTTTTATGATATAAAGAGATACAAAGATTCATAGGAGAAATAGTGGC 1011
Db      294 AlaIlePheProAsnTyrAspProGluLysTyrProIle-----Gly 307
Qy      1012 ATTAACACTGAACTTACAGAGAAATTTATACACTGAAATAAATTTTGACGGCTTACT 1071
Db      308 ValLysSerGluLeuIleArgGluValTyr---ThrAsnValAsnSerAspThrPheArg 326
Qy      1072 TACCTTGAAATTCACCCCAATCTCCTATATGGAATATATTTAAACACGTTTCAGGGCTT 1131
Db      327 -----ThrIleThrGluLeuGluAsnGlyLeuThrArgAsnPro--- 339
Qy      1132 AGATTATTTTCATTTTATGAGTAACTATATTTTATACAAAAT- 1176
Db      340 ThrLeuPheThrTrpIleAsnGlnGlyArgPheTyrThrArgAsnSerArgAspIleLeu 359
Qy      1177 GAAACGTAC-----CGGAATCGTTTGTGTTGTTGCGAATCGTAAAT 1218
Db      360 AspProTyrAspIlePheSerPheThrGlyAsnGlnMetAla----- 373
Qy      1219 AGATCTACTATGCTACGACAGGAAGTGAATATATATGAGAAAGAACAGGT----- 1272
Db      374 ---PheThrHisThrAsnAspAspArgAsnIleIleTrpGlyAlaValHisGlyAsnIle 392
Qy      1273 ---CCACCCCAACAAACCTTTAATACCATTTGAAATCCTAT-----AAAGTT 1317
Db      393 IleSerGlnAspThrSerLysValPheProPheTyrArgAsnLysProIleAspLysVal 412
Qy      1318 TCATTTGTAACCTGATAGACAGTAACCTCTACTTCCCTTTTCTTAACATATATCTTTACA 1377
Db      413 GluIleValArgHisArgGlu-----TyrSerAsp 422
Qy      1378 ATTAATCAATTTGAATTTATTTAAATTAATTCACCTAGTAAATAAATTAAACATATTCAGCT 1437
Db      423 IleIleTyrGluMetIlePhePheSerAsnSer---SerGluValPheArgTyrSerSer 441
Qy      1438 GGGGGGAATTTATCTAATGATAAATAAACAACGATTTTCAATTTCTCTGTAATAAAGAC 1497
Db      442 AsnSerThrIleGluAsnAsnTyrLysArgThrAspSerTyrMetIleProLysGlnThr 461
Qy      1498 TGTAAACCAATTAATTAATCCAAATTTGTTTACCAAGCTATATAAGTTATAGTCATATTTTA 1557
Db      462 TrpLys-----AsnGluGluTyrGlyHisThrLeu 471
Qy      1558 TCCAGATTTTCTTTTATTTAATTTCTATATAAATTTGCGATTGCGCTAAATATATATATAT 1617
Db      472 SerTyrIleLysThrAspAsnTyrIlePheSerVal-----ValArgGluArg 489
Qy      1618 ACAGGTGCATTTAGGATGGACACACAGTAGTGTAAATAGAAATATGCAATATCAGATAAA 1677
Db      489 ArgValAlaPheSerTrpThrHisThrSerValAspPheGlnAsnThrIleAspLeuAsp 508

```

```

Qy      1678 ATAATTCAATGATCCCGCAATCAAGGTAAACAGTCTTGTATACAAAACCTCTAAGTAATT 1737
Db      509 AsnIleThrGlnIleHisAlaLeuLysAlaLeuLysValSerAspSerLysIleVal 528
Qy      1738 GAAGACCTGCTCATACAGAGAGAACTTGTTTATTTTACAAAGTCAAGGGCGTTTAGAG 1797
Db      529 LysGlyProGlyHisThrGlyGlyAspLeuValIleLeuLysAspSer-----MetAsp 546
Qy      1798 ATTACATGTAGA---ACTCCTAATTTCTACACAATCTTTATTATACATTAGACTTCGATCGCT 1854
Db      547 PheArgValArgPheLeuLysAsnValSerArgGlnTyrGlnValArgIleArgTyrAla 566
Qy      1855 ACAATGGTGTGCGAAATACCTCTTCTTAATATATCTCTTACAAATACCAAGGAGTAATAGGA 1914
Db      567 ThrAsnAla-----ProLysThrThrValPheLeuThrGlyIleAspThr 581
Qy      1915 ATACCACCTCAACGACTCAACACACATCTTTCTCGTACAAATTTAAT-----AATTTA 1968
Db      582 IleSerValGlu---LeuProSerThrThrSerArgGlnAsnProAsnAlaThrAspLeu 600
Qy      1969 CAATACGAGATTTGGGTATTTCCAAATTTCCAAAGTACAGTA----- 2010
Db      601 ThrTyrAlaAspPheGlyTyrValThrPheProArgThrValProAsnLysThrPheGlu 620
Qy      2011 -----ACATTACCTTTAAATCGAAACATACCATTTATATTTAATCGTGCAGATGTA 2061
Db      621 GlyGluAspThrLeuLeuMetThr-----LeuTyrGlyThrProAsnHis 635
Qy      2062 TCAATTTCAATTTTAAATCATTTGATAAAATTTGAATTTTATACCAATTTCTCTCTGTACGC 2121
Db      636 SerTyrAsnIle---TyrIleAspLysIleGluPheIleProIleThrGlnSerValLeu 654
Qy      2122 CAAAATAGAGAAAACAAAAATTTAGAAACTATCCAAACAAAAATAAATACATTTTTCACA 2181
Db      655 AspTyrThrGluLysGlnAsnIleGluLysThrGlnLysIleValAsnAspLeuPheVal 674
Qy      2182 AAT 2184
Db      675 Asn 675

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Search completed: January 12, 2006, 06:39:43
Job time : 196 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: January 12, 2006, 06:26:35 ; Search time 9 seconds
(without alignments)

4695.593 Million cell updates/sec

Title: US-10-782-570-1

Perfect score: 3939

Sequence: 1 gtgaatcaaaataataa.....caaaactatgatattgattaa 2235

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 134124

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlpl
-Q=/cgn2_1/USPTO.spool.p/US10782570/runat_12012006_060223_7580/app_query.fasta_1.2375
-DB=Published Applications AA New -QFMT=faстан -SUFFIX=rapbn -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10782570.cgn_1.0 -runat_12012006_060223_7580
-ICPU=6 -ICPU=3 -NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA New.*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pcp.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pcp.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pcp.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pcp.*
5: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pcp.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pcp.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pcp.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	716	18.2	1210	7	US-11-058-727-4
2	716	18.2	1210	7	US-11-108-389-4
3	700	17.8	652	7	US-11-192-801-4
4	699	17.7	1206	7	US-11-058-727-2
5	699	17.7	1206	7	US-11-108-389-2
6	693	17.6	652	7	US-11-192-801-6
7	691	17.5	652	7	US-11-192-801-2
8	683.5	17.4	1386	7	US-11-091-643-6
9	683	17.3	653	7	US-11-192-801-8
10	683	17.3	653	7	US-11-192-801-10

11	683	17.3	653	7	US-11-192-801-12
12	683	17.3	653	7	US-11-192-801-14
13	683	17.3	653	7	US-11-192-801-16
14	683	17.3	653	7	US-11-192-801-18
15	683	17.3	653	7	US-11-192-801-20
16	683	17.3	653	7	US-11-192-801-22
17	683	17.3	653	7	US-11-192-801-24
18	683	17.3	653	7	US-11-192-801-37
19	683	17.3	653	7	US-11-192-801-39
20	675	17.1	673	7	US-11-058-727-14
21	675	17.1	673	7	US-11-108-389-14
22	674	17.1	1316	7	US-11-091-643-4
23	665	16.9	675	7	US-11-058-727-74
24	665	16.9	675	7	US-11-058-727-80
25	665	16.9	675	7	US-11-108-389-74
26	665	16.9	675	7	US-11-108-389-80
27	664.5	16.9	674	7	US-11-058-727-82
28	664.5	16.9	674	7	US-11-108-389-82
29	664	16.9	675	7	US-11-058-727-42
30	664	16.9	675	7	US-11-058-727-48
31	664	16.9	675	7	US-11-108-389-42
32	664	16.9	675	7	US-11-108-389-48
33	663.5	16.8	674	7	US-11-058-727-50
34	663.5	16.8	674	7	US-11-108-389-50
35	662	16.8	673	7	US-11-058-727-70
36	662	16.8	673	7	US-11-108-389-70
37	661	16.8	673	7	US-11-058-727-34
38	661	16.8	673	7	US-11-058-727-68
39	661	16.8	673	7	US-11-108-389-34
40	661	16.8	673	7	US-11-108-389-68
41	660.5	16.8	674	7	US-11-058-727-76
42	660.5	16.8	674	7	US-11-108-389-76
43	660	16.8	673	7	US-11-058-727-22
44	660	16.8	673	7	US-11-058-727-64
45	660	16.8	673	7	US-11-058-727-66

ALIGNMENTS

RESULT 1
US-11-058-727-4
; Sequence 4, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1210
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-058-727-4

Alignment Scores:

Pred. No.:	8, 59e-48	Length:	1210
Score:	716.00	Matches:	216
Percent Similarity:	44.81%	Conservative:	138
Best Local Similarity:	27.34%	Mismatches:	304
Query Match:	18.18%	Indels:	132
DB:	7	Gaps:	30

US-10-782-570-1 (1-2235) x US-11-058-727-4 (1-1210)

Qy	1	GTGAATCAAAATAATAAATGATATGAGATTATCGAATTCAGAGAAATTTATCTATCCT	60
Db	1	MetSerProAsnAsnGlnAsnGluTyrGluIleLeuAspAlaThrProSerThrSerVal	20
Qy	61	TCTAACAGAAATATTGATCTTCTAGATACCTTACACAAATATCCAAATCAACCAATTA	120
Db	21	SerAsn-----AspSerAsnArgTyrProPheAlaAsnGluProThrAsnAlaLeu	37
Qy	121	CAAAACACAAATACAAAGAGTGGCTCAATATGTGTCAAGGGAAT---ACACAATATGGT	177
Db	38	GlnAsnMetAspTyrLysAspPyrLysLeuMetSerAlaGlyAsnAlaSerGluTyrPro	57
Qy	178	GATAATTTTCGACACATTTGCTAGTCTGATACAAATTTGCTGCAGTTAGTGCAGGTACTATT	237
Db	58	GlySerProGluValLeuValSerGlyGlnAsp-----AlaAlaLysAlaAlaLeasp	75
Qy	238	GTATCCGGTACTCTGTAGCCGGTATAGTGGGCTCACTTCTATATCCGACCGATAGGA	297
Db	76	IleValGlyLysLeuLeuSerGlyLeuGly-----ValPro	87
Qy	298	ATAATAGTGTATAATAATATCTTTGGTACCCTCAATCACTGCTTTTGGCCCGCGGA	357
Db	88	PheValGlyProIleValSerLeuTyrThrGlnLeuIleAspIleLeuTyrProSerGly	107
Qy	358	GAACAGACAAACAGTATGGACACAAATTTATTAATAATGGGAGAAATTTTGTGTGATACA	417
Db	108	Gln-----LysSerGlnTyrGluLeuPheMetGluGlnValGluGluLeuLeuAsnGln	125
Qy	418	CCGTTACACAGCAAGCAATAAAGTAAAGTTACAACTTTAGAGGATTTAGACAATA	477
Db	126	LysIleAlaGluTyrAlaArgAsnLysAlaLeuSerGluLeuGluGlyLeuGlyAsnAsn	145
Qy	478	TTACAAAGCTATAATACAGCAATTAGATGATGGAGAAATTTAAAGACTACAGCTCCT	537
Db	146	TyrGlnLeuTyrLeuThrAlaLeuGluTyrLysGlu-----	158
Qy	538	GGATTACCAACCATCATCAGCAATTACAAAGCTGCTTGAATCTTAAATAACGATTTGAG	597
Db	159	-----AsnProAsnGlySer-----ArgAlaLeuArgAspValArgAsnArgPheGlu	174
Qy	598	AATGTTCAATGATTTTATTCGAGAAATACCTGGTTCCAACTTGAACTTAAATAACG	657
Db	175	IleLeuAspSerLeuPheThrGlnTyrMetProSerPheArgValThrAsnPheGluVal	194
Qy	658	CTATTACTACCTATTATGCGCAAGCTGCTAAATTTTCAATTTAAATTTATTAACAACAGGT	717
Db	195	ProPheLeuThrValTyrThrGlnAlaAlaAsnLeuHisLeuLeuLeuLeuLysAspAla	214
Qy	718	GCTGAATTTGGCTGATGAATGGAATGCAGATATACATCTTCCACAAATTTGAACCTAATGCT	777
Db	215	SerIlePheGlyGluGluTyrGlyTyr-----SerThr	225
Qy	778	GGACATCAGATGATATATAAATCTTTAAAGAAATATACCTTAATATAGTAATCTAT	837
Db	226	ThrThrIleAsnAsnTyrTyrAspArgGlnMetLysLeuThrAlaGluTyrSerAspHis	245
Qy	838	TGTGCAAAATCCTATAGAGAGGCTAAATAAATCTTCGAAACGACCTAATATAGATGG	897
Db	246	CysValLysTyrTyrGluThrGlyLeuAlaLysLeuLysGlyThrSerAlaLysGlnTyr	265
Qy	898	AGTATATTATATGATTTTCGAAGATATATGATCTACTTACTGTATTAGTACTTACGTC	957
Db	266	ValAspTyrAsnGlnPheArgGluMetThrLeuThrValLeuAspValValAlaLeu	285

Qy	958	TTTTCTTTTATGATATATAAGAGATACAAAGATTTCAATAGAGAAATAGGTGGCATTTAA	1017
Db	286	PheProAsnTyrAspThrArgThrTyrProMetGlu-----ThrLys	299
Qy	1018	ACTGAACCTTCAAGAGAAATTTTATACAACT-----GAAATAAAATTTTGACCGCTCT	1068
Db	300	AlaGlnLeuThrArgGluValTyrThrAspProLeuGlyAlaValAsnValSerSerIle	319
Qy	1069	---ACTTACCTTGAATTTCAACCCAACTCTCGTATATATGGAATATAATTTAAACAGTTCA	1125
Db	320	GlySerTyrTyrAspLysAlaProSerPheGlyValIleGluSerSerValIleArgPro	339
Qy	1126	GGGCTTAGATATTTTCAATTTTAGTAACTTATTTTATACAAAAAATGAAACG---	1182
Db	340	Pro---HisValPheAspTyrIleThrGlyLeuThrValTyrThrGlnSerArgSerIle	358
Qy	1183	-----TACGGGAATCGTTAGTTGGTATTGCGAATCGTAATAGTACTACTTAT	1230
Db	359	SerSerAlaArgTyrIleArgHisTyrAlaGlyHisGlnIleSerTyrHisArgIlePhe	378
Qy	1231	GCTACGACAGAACTGAAATTTATATATGGAGAAAGAACAGGTCCACCCACACAAAAAAT	1290
Db	379	SerAspAsnIleIleLysGlnMetTyrGlyThrAsnGlnAsnLeuHisSerThrSerThr	398
Qy	1291	TTAATACCATTTGAATCTCTATAAAGTT---TCAATTTGTAAGTATAGACAGAACTCCT	1347
Db	399	---PheAspPheThrAsnTyrAspIleTyrLysThrLeuSerLysAspAlaValLeuLeu	417
Qy	1348	ACTTCCCTTTTCTTAAC-----ATATACTTTTCAATTAATCAAAATGAACTTTAT	1398
Db	418	AspIleValPheProGlyTyrThrTyrIlePhePheGlyMetProGluValGluPhePhe	437
Qy	1399	TTAAATAATTCACCTAGTAAATAAATAACATATTCAGCTGGGGGAAATTTATCTAATGAT	1458
Db	438	MetValAsn-----GlnLeuAsnAsnThr	445
Qy	1459	AAAAAACAACACTGTTTTCAATTTCTGTAAATAAAGACTGTAAACCAATTTT	1512
Db	446	ArgLysThrLeuLysTyrAsn---ProValSerLysAsp-----IleIleAlaGly	461
Qy	1513	-----AATCCAAATTTGTTTACCAGCTATAATAGT	1542
Db	462	ThrArgAspSerGluLeuGluLeuProGluThrSerAspGlnProAsnTyrGluSer	481
Qy	1543	TATAGTCATATTTTATCCAGTTTCTTATTTTATTTATTTTCTATAAAATTTGGATTAGCG	1602
Db	482	TyrSerHisArgLeuCysHisIleThr-----	490
Qy	1603	CTAAATATATATATACAGTGCA-----TTAGATGACACAC	1641
Db	491	---SerIleProAlaThrGlySerThrThrGlyLeuValProValPheSerTyrThrHis	509
Qy	1642	AGTAGTGTAAATAGAAATATCAATATCAGATAAATAATTAACAATGATCCACAGCAATC	1701
Db	510	ArgSerAlaAspLeuIleAsnAlaValHisSerAspLysIleThrGlnIleProValVal	529
Qy	1702	AAAGGTAACAGTCTT-----GATCAAACTCTAAGGTAATTTGAAGGA	1743
Db	530	LysValSerAspLeuAlaProSerIleThrGlyGlyProAsnAsnThrValValSerGly	549
Qy	1744	CTGGGTCAATACAGAGAACTTGGTTTATTTATCAAAAGTCAAGGCGCTTTA-----GAG	1797
Db	550	ProGlyPheThrGlyGlyIleIleLysValIleArgAsnGlyValIleIleSerHis	569
Qy	1798	ATTACATGTAGAATCTCTAATTTCTACACATCTTATTTACATTTAGCTTCCATCGCTACA	1857
Db	570	MetArgValLysIleSerAspIleAsnLysGluTyrSerMetArgIleArgTyrAlaSer	589
Qy	1858	AATGGTCTGGAATATCTCTTCTTAATATATCTTTTACAATACAGGAGTAATAGGAATA	1917
Db	590	-----AlaAsnAsnThrGluPheTyrIleAsnProSerGluGluAsnValLysSer---	606
Qy	1918	CCACCTCAGACTCAACACACTTTTCTGGTGACAAATATTAATTAATTTACAACGGA	1977

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Db      607 HisAlaGlnLysThrMetAsnArgGlyGluAlaLeuThrTyrAsnLysPheAsnTyrAla 626
QY      1978 GATTTGGTATTTCCAAATTTCCAGTACAGTAACTTACCTTTAAATCGAAACATACCA 2037
Db      637 ThrLeuProPheLeuPheThrThrThrGlu-----Pro 638
QY      2038 TTT-----ATATTAATCGTCAGATGTATCAAAATCAATTTTAATCATTT 2082
Db      639 PheIleThrLeuGlyAlaIlePheGluAlaGluAspPheLeuGlyIleGluAlaTyrIle 658
QY      2083 GATAAATGAATTTATACCAATTTCTCTCTGTACGCCAAATPAGAGAAAACAAAAA 2142
Db      659 AspArgIleGluPheIleProValAspGluThrTyr-----GluAlaGluGlnAsp 675
QY      2143 TTGAAACTATCCAAACAAAATAATACATTTTTCACAAATCATACAAAATACTTTA 2202
Db      676 LeuGluAlaAlaLysLysAlaValAsnAlaLeuPheThrAsn---ThrLysAspGlyLeu 694
QY      2203 AATATAGAAGCCCAAACTATGATATTGAT 2232
Db      695 ArgProGlyValThrAspTyrGluValAsn 704

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RESULT 2

US-11-108-389-4

; Sequence 4, Application US/11108389
; Publication No. US20050261188A1

GENERAL INFORMATION:

```

; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4

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Alignment Scores:

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Pred. No.: 8,596-48 Length: 1210
Score: 716.00 Matches: 216
Percent Similarity: 44.81% Conservative: 138
Best Local Similarity: 27.34% Mismatches: 304
Query Match: 18.18% Indels: 132
Db: 7 Gaps: 30

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US-11-108-389-4

; ORGANISM: Bacillus thuringiensis

Alignment Scores:

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Pred. No.: 8,596-48 Length: 1210
Score: 716.00 Matches: 216
Percent Similarity: 44.81% Conservative: 138
Best Local Similarity: 27.34% Mismatches: 304
Query Match: 18.18% Indels: 132
Db: 7 Gaps: 30

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US-10-782-570-1 (1-2235) x US-11-108-389-4 (1-1210)

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QY      1 GTGAATCAAAATAAATAATCAATATGAGATTATCGATTCAAGAAATTTATCTTATCCT 60
Db      1 MetSerProAsnGlnAsnGluThrGluIleAspAlaThrProSerThrSerVal 20
QY      61 TCTAACAGAAATPATTGATCATTTCTAGATACCCCTTACACAAATAATCCAAATCAACCATTA 120
Db      21 SerAsn-----AspSerAsnArgTyrProPheAlaAsnGluProThrAsnAlaLeu 37

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QY      121 CAAACACAAATTAACAAGAGTGGCTCAATATGTGTCAAGGAAT---ACACAATATGCT 177
Db      38 GlnAsnMetAspTyrLysAspTyrLeuLysMetSerAlaGlyAsnAlaSerGluTyrPro 57
QY      178 GATAAATTCGAGACATTTGCTAGTCTGATACAATGTCTGCAGTTAGTGCAGGTACTATT 237
Db      58 GlySerProGluValLeuValSerGlyGlnAsp-----AlaAlaLysAlaAlaIleAsp 75
QY      238 GTATCCGGTACTCTGTGTAGCCGGTATAGTGGGCTCACTTCTATATCCGACCGATAGGA 297
Db      76 IleValGlyLysLeuLeuSerGlyLeuGly-----ValPro 87
QY      298 ATAATAGTGTCTAATAAATATCTTTTGGTACCCTTAATCACTGTCTTTTGGCCCGCGGA 357
Db      88 PheValGlyProIleValSerLeuTyrThrGlnLeuIleAspIleLeuTyrProSerGly 107
QY      358 GAACAAGACAAAACAGTATGACACAAATTTATAAATGGGAGAAATTTTGTGTGATACA 417
Db      108 Gln-----LysSerGlnTyrGluIlePheMetGluGlnValGluGluLeuIleAsnGln 125
QY      418 CCGTTAACAGAAAGCATAAACAGCTAAAGTTACAACTTTTAGAGGATTTAGACAATA 477
Db      126 LysIleAlaGluTyrAlaArgAsnLysAlaLeuSerGluLeuGluGlyLeuGlyAsnAsn 145
QY      478 TTACAAAGCTATATACAGCATTAGATGATTGGAGAAATTAATAAAGAGACTACAAGCTCCT 537
Db      146 TyrGlnLeuTyrLeuThrAlaLeuGluGluTyrLysGlu----- 158
QY      538 GGATTACCAACCATCATCAGCATTTACAACAGCTGCTTTGACTCTTTAAATACGATTGAG 597
Db      159 -----AsnProAsnGlySer-----ArgAlaLeuArgAspValArgAsnArgPheGlu 174
QY      598 AATGTTCAATGATTTTATTCGAGAAATATACCTGTTTCCAACTTGAACCTTATAAAGC 657
Db      175 IleLeuAspSerLeuPheThrGlnTyrMetProSerPheArgValThrAsnPheGluVal 194
QY      658 CTATTACTACTTATTATGCGCAAGCTGCTAATTTTCAATTTTAAATTTTATTACAAAGGT 717
Db      195 ProPheLeuThrValTyrThrGlnAlaAlaAsnLeuHisLeuLeuLeuLeuLysAspAla 214
QY      718 GCTGAATTTGGTGAATGGAATGCAGATATACATCTTCCAAATTTCAAAATGAACTAATGCT 777
Db      215 SerIlePheGlyGluGluTyrGlyTrp-----SerThr 225
QY      778 GGAACATCAGATGACTATTATAAATTTTAAAGAAATATACCTTAATATAGTAACTAT 837
Db      226 ThrThrIleAsnAsnTyrTyrAspArgGlnMetLysLeuThrAlaGluTyrSerAspHis 245
QY      838 TGTGCAATACCTATAGAGAAGGACTAAATAAATCTTCGAAACGAACTTAATATGAGATGG 897
Db      246 CysValLysTyrTyrGluThrGlyLeuAlaLysLeuLysGlyThrSerAlaLysGlnTyr 265
QY      898 AGTATATTATTAATGATATATCGAAGATATATGACTATTACTGTATTAGATATATCGCTCAA 957
Db      266 ValAspTyrAsnGlnPheArgArgGluMetThrLeuThrValLeuAspValValAlaLeu 285
QY      958 TTTTCTTTTATGATATAAAGAGATACAAGATTCATAGAGAAATAGGTGGCAATTAAA 1017
Db      286 PheProAsnTyrAspThrArgThrTyrProMetGlu-----ThrLys 299
QY      1018 ACTGAACCTTACAGAGAAATTTATCAACT-----GAAATAAATTTTGACCGCTCTT 1068
Db      300 AlaGlnLeuThrArgGluValTyrThrAspProLeuGlyAlaValAsnValSerSerIle 319
QY      1069 ----ACTTACCTTTGAAATTAACCCCACTCTCGCTATAATGGAATATAATTTTAAACGTTCA 1125
Db      320 GlySerTyrAspLysAlaProSerPheGlyValIleGluSerSerValIleArgPro 339
QY      1126 GGGCTTAGATTATTTCATTTTATAGTGAACCTTATTTATTTATTAACAAAATAAAGACG--- 1182
Db      340 Pro---HisValPheAspTyrIleThrGlyLeuThrValTyrThrGlnSerArgSerIle 358

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QY 1183 -----TACGGGAATCGTTTGTAGTTGGTATTCGGAATCGTAATAGATCTACTTAT 1230
Db |||||
QY 359 SerSerAlaArgTyrIleArgHisTrpAlaGlyHisGlnIleSerTyrHisArgIlePhe 378
Db |||||
QY 1231 GCTACGACAGGAACCTGAATATATATATGAGAAAGACAGAGTCCACCCACACAAACAAACT 1290
Db |||||
QY 379 SerAspAsnIleIleLysGlnMetTyrGlyThrAsnGlnAsnLeuHisSerThrSerThr 398
Db |||||
QY 1291 TTAATACACTTGAATCCTTAAGTT---TCAATTGTAACTGTAGTACAAAGTAAGTACTCCT 1347
Db |||||
QY 399 ---PheAspPheThrAsnTyrAspIleTyrIlePheGlyMetProGluValGluPhePhe 417
Db |||||
QY 1348 ACTTCCCTTTTCCCTAAC-----ATATACTTTTACAATTAATCAAAATGAAGCTTTAT 1398
Db |||||
QY 418 AsplleValPheProGlyTyrThrTyrIlePhePheGlyMetProGluValGluPhePhe 437
Db |||||
QY 1399 TTAATAATATCACCTAGTAATAATAATTAACATATTCAGCTGGGGGAAATTTATCTAATGAT 1458
Db |||||
QY 438 MetValAsn-----GlnLeuAsnAsnThr 445
Db |||||
QY 1459 AAAAAACACAGTATTTCAATTTCTGTAAAAAAGACGTGAACCAATATT----- 1512
Db |||||
QY 446 ArgLysThrLeuLysTyrAsn---ProValSerLysAsp-----IleIleAlaGly 461
Db |||||
QY 1513 -----AATCCAAATTTGTTACCAAGCTTAATAGT 1542
Db |||||
QY 462 ThrArgAspSerGluLeuGluLeuProProGluThrSerAspGlnProAsnTyrGluSer 481
Db |||||
QY 1543 TATAGTCATATTTTATCCAGTTTCTTTTATTTTATTTATTTATTTATTTATTTATTTATTTATTT 1602
Db |||||
QY 482 TyrSerHisArgLeuCysHisIleThr----- 490
Db |||||
QY 1603 CTAATATATATATATACAGGTGCA-----TTAGGATGGACACAC 1641
Db |||||
QY 491 ---SerIleProAlaThrGlySerThrThrGlyLeuValProValPheSerTrpThrHis 509
Db |||||
QY 1642 AGTAGTGTATAGAAATAGCAATATATCAATATAATTAATCAATATCCAGCAATC 1701
Db |||||
QY 510 ArgSerAlaAspLeuIleAsnAlaValHisSerAspLysIleThrGlnIleProValVal 529
Db |||||
QY 1702 AAAGTAAACAGTCTT-----GATACAAACTCTAAAGTAAATGAAGCA 1743
Db |||||
QY 530 LysValSerAspLeuAlaProSerIleThrGlyGlyProAsnAsnThrValValSerGly 549
Db |||||
QY 1744 CTGTGTCATACGAGGAACCTGTTGTTATTTTACAAAGTCAAGGCGTTTA-----GAG 1797
Db |||||
QY 550 ProGlyPheThrGlyGlyIleIleLysValIleArgAsnGlyValIleIleSerHis 569
Db |||||
QY 1798 ATTACATGTAGAACTCCTAATTTCTACAACTTATTACATTTAGACTTCGATACGCTACA 1857
Db |||||
QY 570 MetArgValLysIleSerAspLysGluTyrSerMetArgIleArgTyrAlaSer 589
Db |||||
QY 1858 AATGTGTCTGGAATACTCTTCTAATATATCTTCTTACAAATACCAAGGAGTAAATAGGAATA 1917
Db |||||
QY 590 -----AlaAsnAsnThrGluPheTyrIleAsnProSerGluGluAsnValLysSer--- 606
Db |||||
QY 1918 CCACCTCAACGACTCAACACACTTTTCTGGTACAAATTAATAATTTTACAATACGGA 1977
Db |||||
QY 607 HisAlaGlnLysThrMetAsnArgGlyGluAlaLeuThrTyrAsnLysPheAsnTyrAla 626
Db |||||
QY 1978 GATTTTGGGTATTTCCCAATTTCCAGTACAGTACATTTACTCTTTAATTCGAAACATACCA 2037
Db |||||
QY 627 ThrLeuProProIleLysPheThrThrThrGlu-----Pro 638
Db |||||
QY 2038 TTT-----ATATTTAATCGTGCAGATGTATCAAAATTTCAATTTTAAATCAATT 2082
Db |||||
QY 639 PheIleThrLeuGlyAlaIlePheGluAlaGluAspPheLeuGlyIleGluAlaTyrIle 658
Db |||||
QY 2083 GATAAAATGAATTTATACCAATTTACTTCTGTACGCCAAAATAGAGAAAACAAAA 2142
Db |||||
QY 659 AspArgIleGluPheIleProValAspGluThrTyr-----GluAlaGluGlnAsp 675
Db |||||
QY 2143 TTAGAAACTATCCAAACAAAAATAATACATATTTTTCACAAATCATACAAAAAATCTTTA 2202
Db |||||
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Db 676 LeuGluAlaLysLysAlaValAsnAlaLeuPheThrAsn---ThrLysAspGlyLeu 694
QY 2203 AATATAGAGCCACAAACTATGATATTGAT 2232
Db |||||
QY 695 ArgProGlyValThrAspTyrGluValAsn 704
Db |||||
RESULT 3
US-11-192-801-4
; Sequence 4, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/11/192,801
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/10/232,665
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-192-801-4
Alignment Scores:
Pred. No.: 1,31e-46 Length: 652
Score: 700.00 Matches: 216
Percent Similarity: 44.58% Conservative: 117
Best Local Similarity: 28.92% Mismatches: 272
Query Match: 17.77% Indels: 142
DB: 7 Gaps: 32
US-10-782-570-1 (1-2235) x US-11-192-801-4 (1-652)
QY 1 GTGAATCAAAATAATAATAATGAATATGAGATTATCGAT---TCAAAAGAAATTTATCTTAT 57
Db |||||
QY 1 MetAsnProAsnAsnArgSerGluHisArgThrIleLysValThrProAsnSerGluLeu 20
Db |||||
QY 58 CTTCTTAACAGAAATATTTGATTCATCTAGATACCTTACACAAATATCCAAATCAACCA 117
Db |||||
QY 21 ProthrAsn-----HisAsnGlnTyrProLeuAlaAspAsnProAsnSerThr 36
Db |||||
QY 118 TTACAAACACAAATTAACAAGAGTGGCTCAATATGTGTCAA---GGGAATACAAATAT 174
Db |||||
QY 37 LeuGluGluLeuAsnTyrLysGluPheLeuArgMetThrGluAspSerSerThrGluVal 56
Db |||||
QY 175 GGTGATATTTTCGAGACATTTGCTAGTCTGCTGATACAAATGTCT---GCAGTTAGTCAGGT 231
Db |||||
QY 57 LeuAspAsn-----SerThrValLysAspAlaValGlyThrGly 69
Db |||||
QY 232 ACTATTGTATCCGGTACTCTGTAGCCGGTATAGTGGGCTCACTTCTATATATCGGACCG 291
Db |||||
QY 70 IleSerValValGlyGlnIleLeuGlyValValGly----- 81
Db |||||
QY 292 ATAGGAATAATAGTGTCTAATAATAATATCTTTGGTACCCTCAATCACTGTCTTTTGGCCC 351
Db |||||
QY 82 ValProPheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAspThrIleTrpPro 101
Db |||||
QY 352 GCGGAGAACACAGACAAACAGATGTGACACAAATTTATTAAATGGGAGAAATTTTGT 411
Db |||||
QY 102 Ser-----AspAlaAspProTrpLysAlaPheMetAlaGlnValGluValLeuIle 118
Db |||||
QY 412 GATACACCGTTACAGAAAGCATAAAGCAGTTAAGTTACAACTTTAGAGAGTTAGA 471
Db |||||
QY 119 AspLysIleGluGluTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGln 138
Db |||||
QY 472 CAAATATTACAAAGCTAATAATACAGCATTAGATTGGAGAAATTTAAAAAGACTACAA 531
Db |||||
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139 AsnAsnPheGluAspTyrValAsnAlaLeuAsnSerTrpLysLys----- 153
Qy GCTCCTGATATACACCATCATCAGCATTAACAACAGCTGCTTAAATACGA 591
Db -----ThrProLeuSerLeuArgSerLysArgSerGlnAspArgLysLeu 170
Qy TTTGAGAAATGTTCAATGATTTATTCGAGAAATACCTGCTTCCCAATCGAACTTAT 651
Db -----PheSerGlnAlaGluSerHisPheArgAsnSerMetProSerPheAlaValSerLysPhe 190
Qy AAAACGCTATTATACCTATTATGCGCAAGCTGCTAAATTTTCATTTAAATTTATACAA 711
Db -----GluValLeuPheLeuProThrTyrAlaGlnAlaAlaAsnThrHisLeuLeuLeuLys 210
Qy CAAGTGTGTAATGGCTGATGAATGGAAATGCAGATATACCTTCACAAATGAACTT 771
Db -----AspAlaGlnValPheGlyGluGluTrpGlyTyrSer----- 222
Qy AATGCTGGAACATCAGATGACTATTATAAACTTTTAAAGAAATATACCTAAATATAGT 831
Db -----SerGluAspValAlaGluPheTyrHisArgGlnLeuLysLeuThr---GlnGlnTyrThr 241
Qy AACTATTGTGCAATACCTATAGAGAGAGACTAAATAAACTTCGAAACGAACCTAATATG 891
Db -----AspHisCysValAsnTrpTyrAsnValGlyLeuAsnGlyLeuArgGlySerThrTyrAsp 261
Qy AGATGGAGTATTATTAAGTATTTCGAAGATATATGACTATTATCTGTTATAGATATATC 951
Db -----AlaTrpValLysPheAsnArgPheArgGluMetThrLeuThrValLeuAspLeuIle 281
Qy GCTCAATTTCTTTTATGATATAAGAGATACAAAGATTCATAGGAAGATAGGTGGC 1011
Db -----ValLeuPheProPheTyrAspValArgLeuTyrSerLys-----Gly 295
Qy ATTTAACTGAACTTACAGGAATTTATACAACTGAAATAAATTTTGACGCTTACT 1071
Db -----ValLysThrGluLeuThrArgAspPheThrAspProIle---PheSerLeuAsnThr 314
Qy TACCTTGAATTCACCAATCTCGTATATATGGAATATATTTAAACAGTTCAGGGCTT 1131
Db -----LeuGlnGluTyrGlyProThrPheLeuSerIleGluAsnSerIleArgLysPro----- 332
Qy AGATTATTTTCTATTTAGTGAACCTATATTTTATACAAA----- 1173
Db -----HisLeuPheAspTyrLeuGlnGlyIleGluPheHisThrArgLeuGlnProGlyTyrSer 352
Qy -----AATGAAACGTACGGGAATCGTTTGTGTTATTCGGAATCGTAAT 1218
Db -----GlyLysAspSerPheAsnTyrTrpSerGlyAsnTyr-----ValGluThrArgPro 369
Qy AGATCTATCTATGCTACGACGAACTGMAATATATATATGGAAGAAGACAGGTCCACC 1278
Db -----SerIleGlySerSerLysThrIleThrSerProPheTyrGlyAspLysSerThrGluPro 389
Qy ACAACAAACAACTTTAATCCATTCATCTAATAAGTTCAATGTTAATGATAGACAA 1338
Db -----ValGlnLys-----LeuSerPheAspGlyGlnLysValTyr-----ArgThr 403
Qy GTA-----ACTCTACTTCCCTTTTCTCTAC-----ATATACTTTTACAAATTAATCA 1386
Db -----IleAlaAsnThrAspValAlaAlaTrpProAsnGlyLysIleTyrPheGlyValThrLys 423
Qy ATGCACTTTTAAATAATTAATTCACCTAGTATAAATTA-----ACATATTCAGCT 1437
Db -----ValAspPheSerGlnTyrAspAspGlnLysAsnGluThrSerThrGlnThrTyrAspSer 443
Qy -----GGGGGAATTTTATCTAATGATAAA-----AAAAA 1467
Db -----LysArgAsnAsnGlyHisValGlyAlaGlnAspSerIleAspGlnLeuProGluThr 463
Qy ACTGATTTTCAATTTCTCTGTAAGAAAGACTGTAACCAATTTATTAATCAAAATTTT 1527
Db -----GluProLeuGluLys----- 470

1528 CCAAGCTATAATAGTATAGTATATTTATTCCTCCAGTTTCTTTATTTAATTTATTCCTAT 1587
Qy -----AlaTyrSerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGlnAsp 486
Db -----ArgArgGlyThrIle-----ProPhePheThr-----TrpThrHisArgSer 500
Qy GTTAAATAGAAATATGCAATATCAGATAAAATATTAATGATCCAGCAATCAAAAGT 1707
Db -----ValAspPhePheAsnThrIleAspAlaGlnLysIleThrGlnLeuProValLysAla 520
Qy AACAGTCTTGATACAACTCTAAGCTAATTAAGAGCACTGCTCATACAGGAGGAACTTG 1767
Db -----TyrAlaLeuSerSerGlyAlaSerIleIleGluGlyProGlyPheThrGlyGlyAsnLeu 540
Qy GTTTATTTTACAA-----AGTCAAGGGCGTTTATAGATTTACATGTAGAACTCCT 1815
Db -----LeuPheLeuLysGluSerSerAsnSerIleAlaLysPheLysValThrLeuAsnSerAla 560
Qy AATTCTACACATCTTATTACATTTAGACTTCGATCGTACATAAATGGTGTGGAATACT 1875
Db -----AlaLeuLeuGlnArgTyrArgValArgIleArgTyrAlaSerThr----- 575
Qy CTTCCTAATATCTCTTACAAATACAGGAGTAAATAGGAATACCACTCAACGACTCAAC 1935
Db -----ThrAsnLeuArgLeuPheVal-----GlnAsnSerAsn 586
Qy AACACTTTTCTGCTACAAATTTAATAATTTACAATAC-----GGAGATTTTGGGTAT 1989
Db -----AsnAspPheIleValIleTyrIleAsnLysThrMetAsnIleAspAspLeuThrTyr 606
Qy TTCCAATTTCCAGTACAGTAACTTACTTTAATTCGAACATACCACTT----- 2040
Db -----GlnThrPheAspLeuAlaThr-----AsnSerAsnMetGlyPheSerGlyAsp 623
Qy -----ATATTTAATCGTGCAGATGTATCAAAATTCAAATTTCAATTTAATCATTTAT 2085
Db -----ThrAsnGluLeuIleIleGlyAlaGluSerPheValSerAsnGluLysIleTyrIleAsp 643
Qy AAAATTGAATTTATACCAAT 2106
Db -----LysIleGluPheIleProVal 650
RESULT 4
US-11-058-727-2
; Sequence 2, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; PRIORITY FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIORITY FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIORITY FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIORITY FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2

Db 320 GlySerTrpTyrAspLysAlaProSerPheGlyValIleGluSerSerValIleArgPro 339
 QY 1126 GGCCTTAGATATTTTCATTTTATAGTCACTTATATTTTATACAAAATAAGAAACGTAC 1185
 Db 340 Pro----HisValPheAspTyrIleThrGlyLeuThrValTyrThrGlnSerArgSerIle 358
 QY 1186 GGGAAAT---CGTTAGTTGGTATTGCGAATCCTAATAGATCTACTTAT---GCTACG 1236
 Db 359 SerSerAlaAlaGlyTyrIleArgHisTrpAlaGlyHisGlnIleSerTyrHisArgValSer 378
 QY 1237 ACAGAACTGAAATTT-----ATATATGGAGAAAGAACAGGTCCACCCACACAAACAACT 1290
 Db 379 ArgGlySerAsnLeuGlnGlnMetTyrGlyThrAsnGlnAsnLeuHisSerThrSerThr 398
 QY 1291 TTAATACCATTTGAATCTCTATAAAGTT---TCATTTGTAACGTATAGACAAAGTAACTCCT 1347
 Db 399 ---PheAspPheThrAsnTyrAspIleTyrLysThrLeuSerLysAspAlaValLeuLeu 417
 QY 1348 ACTTCCCTTTTCCTAAC-----ATATACTTTTACAATTAATCAAAATTTGAATTTAT 1398
 Db 418 AspIleValTyrProGlyTyrThrTyrIlePhePheGlyMetProGluValGluPhePhe 437
 QY 1399 TTAATAAATCACCTAGTAATAAATAATTAACATTAATTCAGCTGGGGGAATTTATCTAATGAT 1458
 Db 438 MetValAsn-----GlnLeuAsnAsnThr 445
 QY 1459 AAAAAACAACTGATTTTCAATTTCTGTAAAAAGAGCTGTAAACCAATTTAATATCCA 1518
 Db 446 ArgIlyThrLeuLysTyrAsn---ProValSerLysAspIleIleAlaSerThrArgAsp 464
 QY 1519 AATTGTTTA-----CCAAGCTATAATAGTTATAGTCAT 1551
 Db 465 SerGluLeuGluLeuProGluThrSerAspGlnProAsnTyrGluSerTyrSerHis 484
 QY 1552 ATTTATCCAGTTTCTTTTATTTAATTTATTCCTATAAAATTTGGATTAGCGCTAAATATA 1611
 Db 485 ArgLeuCysHisIleThr-----SerIle 492
 QY 1612 TTATATACAGCT-----GCATTAGAGTGCAGACACAGTAGTGT 1650
 Db 493 ProIaThrGlyAsnThrThrGlyLeuValProValPheSerTrpThrHisArgSerAla 512
 QY 1651 AATAGAATAATGCAATATCAGATAAATAATTAACAATATCCAGCAATCAAAAGGTAAC 1710
 Db 513 AspLeuAsnAsnThrIleTyrSerAspLysIleThrGlnIleProAlaValIleCysTrp 532
 QY 1711 AGCTTTGATCAAACTCTAAGGTAATTAAGAGACTGGTCTATACAGGAGGAACTGGTT 1770
 Db 533 AspAsnLeuProPheValProValValLysGlyProGlyHisThrGlyGlyAspLeuLeu 552
 QY 1771 ---TATTTACAAAGCTCAAGGG-----CGT 1791
 Db 553 GlnTyrAsnArgSerThrGlySerValGlyThrLeuPheLeuAlaArgTyrGlyLeuAla 572
 QY 1792 TTAGAGATTACATGTAGAAGCTCTAAATCTTACACAACTCTATTATTCATTTAGACTTCGATAC 1851
 Db 573 LeuGlu-----LysAlaGlyLysTyrArgValArgValGluArgTyr 585
 QY 1852 GCTCAAAATGGTGTGGAAATFACCTTCTCTAATATCTCTTACAAATCCAGGAGTAAATA 1911
 Db 586 AlaThrAspAla-----AspIleValLeuHisValAsnAspAlaGln 599
 QY 1912 GGAATACCACTCAACGACTCAACACACACTTTTCTGTGTACAAATTAATAATTTACAA 1971
 Db 600 IleGlnMetProLysThrMetAsnProGly-----GluAspLeuThr 613
 QY 1972 TACGAGATTTTGGTATTTCCAAATTTCCAAAGTACAGTAAACATTACCTTTTAAATCGAAAC 2031
 Db 614 SerLysThrPheLysValAlaAspAlaIleThrThrLeuAsnLeuAlaThrAspSerSer 633
 QY 2032 ATACCATTTATTTAATCGGACAGATGTATCAAAATTTCA-----ATTTTAATC 2079
 Db 634 LeuAlaLeuLysHisAsnLeuGlyGluAspProAsnSerThrLeuSerGlyIleValTyr 653

QY 2080 ATTGATAAATTTGATTTATATACCAATTTACTTCTCTGTACGCCAAATAGAGAAAACAA 2139
 Db 654 ValAspArgIleGluPheIleProValAspGluThrTyr-----GluAlaGluGln 670
 QY 2140 AAATTAGAAACTATCCAAACAAATAAATACATATTTTTCACAAATCATACAAAAAATACT 2199
 Db 671 AspLeuGluAlaIleLysAlaValAsnAlaLeuPheThrAsn---ThrLysAspGly 689
 QY 2200 TTAATAATAGAACCCAAACTATGATATTGAT 2232
 Db 690 LeuArgProGlyValThrAspTyrGluValAsn 700
 RESULT 6
 US-11-192-801-6
 ; Sequence 6, Application US/11192801
 ; Publication No. US20050273882A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Romano, Charles P.
 ; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
 ; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
 ; CURRENT APPLICATION NUMBER: US/11/192,801
 ; PRIOR FILING DATE: 2005-07-29
 ; PRIOR APPLICATION NUMBER: US/10/232,665
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US/09/377,466
 ; PRIOR FILING DATE: 1999-08-19
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 652
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic or
 ; FEATURE: non-naturally occurring amino acid sequence encoded by SEQ ID NO:
 ; NAME/KEY: PRT
 ; LOCATION: (1)..(652)
 ; US-11-192-801-6
 Alignment Scores:
 Pred. No.: 4-5e-46 Length: 652
 Score: 693.00 Matches: 208
 Percent Similarity: 44.84% Conservative: 122
 Best Local Similarity: 28.26% Mismatches: 286
 Query Match: 17.59% Indels: 120
 DB: 7 Gaps: 28
 US-10-782-570-1 (1-2235) x US-11-192-801-6 (1-652)
 QY 1 GTCGAATCAAAATAATTAATGAATATGAGATTATCGATTCAAGAATTTATCTTATCTCT 60
 Db 1 MetAsnProAsnAsnArgSerGluHisAspThrIle-----LysValThrProAsn 17
 QY 61 TCTAACAGAAATATTGATCTTCTAGTACCTTACACAAATATCAAAATCAACCAATTA 120
 Db 18 SerGluLeuGlnThrAsnHisAsnGlnTyrProLeuAlaAspAsnProAsnSerThrLeu 37
 QY 121 CAAACACACAAATTAACAAAGAGTGGCTCAATATGTGTCAA---GGGAATACACAATATGGT 177
 Db 38 GluGluLeuAsnTyrLysGluPheLeuArgMetThrGluAspSerSerThrGluValLeu 57
 QY 178 GATAAATTCGAGACATTTTGTCTAGTGTGATACAAATTTGCT---GCAGTTAGTCAGGTPACT 234
 Db 58 AspAsn-----SerThrValLysAspAlaValGlyThrGlyIle 70
 QY 235 ATTGTATCCGGTACTCTGTTAGCCGGTATAGTGGGCTCACTTCTATATCCGACCGATA 294
 Db 71 SerValValGlyGlnIleLeuGlyValValGly-----Val 82
 QY 295 GGAATAATAGTGTCTATAATAATATCTTTTGGTACCTCAATCACTGTCTTTTGGCCGCG 354

Db 83 PropheAlaGlyAlaLeuThrSerPheTyGlnSerPheLeuAenThrIleTrpProSer 102
QY 355 GGAGAACAGACAAACAGTAGTGGACAAATTTATTAATAATGGGAGAAATTTTGTTCAT 414
Db 103 -----AspAlaAspProTrpLysAlaPheMetAlaGlnValGluValLeuIleAsp 119
QY 415 ACACGGTTAAACAGAACGATCAACAGCTAAAGTTTACAACTTTTGAAGAGGATTTAGACAA 474
Db 120 LysLysIleGluGluTyAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAen 139
QY 475 ATATTACAAAGCTAATAACAGCATTAGATGATGAGAAATTTAAAGAGCTACAGCT 534
Db 140 AenPheGluAspTyValAenAlaLeuAenSerTrpLysLys----- 153
QY 535 CTGGATTACACCACTATCAGCATTAACAACAGCTGCTTGAATCTTAAATACGATTT 594
Db 154 -----ThrProLysSerLeuArgSerLysArgSerGlnAspArgIleArgGluLeuPhe 171
QY 595 GAGATGTTCAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAACCTTATATAA 654
Db 172 SerGlnAlaGluSerHisPheArgAenSerMetProSerPheAlaValSerLysPheGlu 191
QY 655 AGCTATTATACCTATTATGCGCAAGCTGCTAAATTTTCAATTTTAAATTTTATTAACAA 714
Db 192 ValLeuPheLeuProThrTyAlaGlnAlaAenThrHisLeuLeuLeuLeuLysAsp 211
QY 715 GGTGCTGAATGGCTGATGAATGGAATGCAGATATACATCTTCACAAATTCGAACCTAAT 774
Db 212 AlaGlnValPheGlyGluGluTrpGlyTyrSer-----Ser 223
QY 775 GCTGGAACATCAGATGACTATTATAAACTTTTAAAGAAATATATACCTTAAATATAGTAAC 834
Db 224 GluAspValAlaGluPheTyHisArgGlnLeuLysLeuThr--GlnGlnTyThrAsp 242
QY 835 TATTGTCAAATACCTATAGAGAGGACTAAATAAATCTTGAACAGAACCTTAATATAGAGA 894
Db 243 HisCysValAenTrpTyrAsnValGlyLeuAenGlyLeuArgGlySerThrTyrAspAla 262
QY 895 TGGAGTATATTATGATTATCGAGATATATGACTATTATCTGATTTATAGATACCTATCGCT 954
Db 263 TrpValLysPheAsnArgPheArgGluMetThrLeuThrValLeuAspLeuIleVal 282
QY 955 CAATTTCTTTTATGATATAAGAGATACAAAGATTCATAGGAAGATAGGTGGCAT 1014
Db 283 LeuPheProPheTyAspIleArgLeuTySerLys-----GlyVal 296
QY 1015 AAACTGAACCTTACAGAGAAATTTATACAACTGAAATTAATTTTTCGCGCTTACTTAC 1074
Db 297 LysThrGluLeuThrArgAspIlePheThrAspProIle---PheSerLeuAenThrLeu 315
QY 1075 CTTGAAATTCACCCCAATCTCGCTATATATGATATATTAACAGCTTCAGGGCTTAGA 1134
Db 316 GlnGluTyGlyProThrPheLeuSerIleGluAenSerIleArgLysPro-----His 333
QY 1135 TTATTTTCATTTTATAGTGAATTTATTTATATATATATATATATATATATATATATATAT 1173
Db 334 LeuPheAspTyLeuGlnGlyIleGluPheHisThrArgLeuGlnProGlyTyPheGly 353
QY 1174 -----AATGAAACGTCACGGGAATCGTTTATGTTGGTATTCGGAATCGTAATAGA 1221
Db 354 LysAspSerPheAsnTyTrpSerGlyAsnTy-----ValGluThrArgProSer 370
QY 1222 TCTACTTATGTCACAGAGGAACTGAAATTTATATATGAGAGAAAGACAGGTCCACCCACA 1281
Db 371 IleGlySerSerLysThrIleThrSerProPheTyGlyAspLysSerThrGluProVal 390
QY 1282 ACACAAACTTTAATACCACTTCAATCTTATATGATTTCAATGTTGATGATAGACAGTA 1341
Db 391 GlnLys-----LeuSerPheAspGlyGlnLysValTy-----ArgThrIle 404
QY 1342 -----ACTCCTACTTCCCTCTTTTCCCTAAC-----ATATACCTTTACAATTAATCAAT 1389
Db 405 AlaAenThrAspValAlaAlaTrpProAenGlyLysValTyLeuGlyValThrLysVal 424

QY 1390 GAACCTTTTAAATAATTCACCTAGTAATAAATTA-----ACATATTTCAGCT--- 1437
Db 425 AspPheSerGlnTyArgAspAspGlnLysAenGluThrSerThrGlnThrTyAspSerLys 444
QY 1438 -----GGGGGGAATTTATCTAATGATAAAAAACAACGATTTTCAATTTCTCTGTA 1491
Db 445 ArgAenAenGlyHisValSerAlaGlnAspSerIleAsp-----GlnLeuProGlu 462
QY 1492 AAAGACTGTAACCAATTTAATCCAAATTTGTTTCCACGCTATATATAGTATAGTCAT 1551
Db 463 ThrThrAspGluProLeu-----GluLysAlaLysSerHis 474
QY 1552 ATTTTATCCCAAGTTTCTTTTATTTAATTTATCTTATAAATTCGATAGCGCTAAATATA 1611
Db 475 GlnLeuAenTyAlaGluCysPheLeuMetGlnAspArgArgGlyThrIle-----Pro 492
QY 1612 TTATATACAGCTGATAGGATGACACACAGTAGTGTGTTAATAGAAATTAATGCAATATCA 1671
Db 493 PhePheThr-----TipThrHisArgSerValAspPhePheAenThrIleAsp 508
QY 1672 GATAAAATTAATCAATGATCCAGCAATCAAGGTAACAGCTCTTGATACAACTCTAAG 1731
Db 509 AlaGluLysIleThrGlnLeuProValLysAlaTyAlaLeuSerSerGlyAlaSer 528
QY 1732 GTAAATTGAAGACCTGGTCATACAGAGGAACTTGGTTTATTTTACAA----- 1779
Db 529 IleIleGluGlyProGlyPheThrGlyGlyAenLeuLeuPheLeuLeuGluSerSerAen 548
QY 1780 AGTCAAGGCGCTTAGAGATTACATGTAGAACTCTCTAATCTTACACAACTTTATTCATT 1839
Db 549 SerIleAlaLysPheLysValThrLeuAenSerAlaAlaLeuLeuGlnArgTyArgVal 568
QY 1840 AGACTTCGATACGCTCAAAATGGTCTGGAATACTCTCTCTAATATATCTCTTACAATA 1899
Db 569 ArgIleArgTyAlaSerThr-----ThrAenLeuArgLeuPheVal 582
QY 1900 CCAGGAGTAATAGGAATACCACTCAACGCTCAACACACTTTTCTGTTACAAATATAT 1959
Db 583 -----GlnAenSerAenAenAspPheLeuValIleTyIle 594
QY 1960 AAT-----AATTACAAATACGAGATTTTGGGTATTTTCCAATTT 1998
Db 595 AenLysThrMetAenLysAspAspLeuThrTyAenThrPheAspLeuAlaThrThr 614
QY 1999 CCAAGTACAGTAACATTTACCTTTAAATCGAAACATACCATTTATATTTAATGTCGACAT 2058
Db 615 AenSerAenMetGlyPheSerGlyAspLysAenGluLeuIleIleGlyAlaGluSerPhe 634
QY 2059 GTATCAAAATTTCAATTTAATCATGATAAATTTGAATTTATATATATATATATATAT 2106
Db 635 ValSerAenGluLysIleTyIleAspLysIleGluPheIleProVal 650

RESULT 7

US-11-192-801-2
; Sequence 2, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/11/192,801
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/10/232,665
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis

US-11-192-801-2

Alignment Scores:

Pred. No.: 6,41e-46 Length: 652
 Score: 691.00 Matches: 208
 Percent Similarity: 44.84% Conservative: 122
 Best Local Similarity: 28.26% Mismatches: 286
 Query Match: 17.54% Indels: 120
 DB: 7 Gaps: 28

US-10-782-570-1 (1-2235) x US-11-192-801-2 (1-652)

QY 1 GTGAATCAAAATAAATAAATAATGAGATTATCGATTCAAAGAAATTTATCTTATCCT 60
 DB 1 MetAbnProAbnAaSerGluHisAspThrIle-----LysValThrProAbn 17
 QY 61 TCTAAACAGAAATATTGATCATCTAGATACCCCTTACACAAATAATCCAAATCAACCAATTA 120
 DB 18 SerGluLeuGlnThrAsnHisAsnGlnTyrProLeuAlaAspAsnProAbnSerThrLeu 37
 QY 121 CAAACACAAATTAACAAAGAGTGGCTCAATATGTGCTCAA-----GGGAATACAAATATGCT 177
 DB 38 GluGluLeuAsnTyrLysGluPheLeuArgMetThrGluAspSerSerThrGluValLeu 57
 QY 178 GATTAATTCGAGACATTTGCTAGTCTGATACAATTGCT---GCAGTTAGTGCAGGTACT 234
 DB 58 AspAsn-----SerThrValLysAspAlaValGlyThrGlyIle 70
 QY 235 ATTGATCCGGTACTCTGTTAGCCGGTATAGTGGGCTCACTTCTATATCCGACCCGATA 294
 DB 71 SerValValGlyGlnIleLeuGlyValValGly-----Val 82
 QY 295 GGAATAATAGTGGCTATATAATATATCTTTTGGTACCCTAATCACTGCTCTTTGGCCGCG 354
 DB 83 ProPheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnThrIleTrpProSer 102
 QY 355 GGAGAACAGACAAACAGTAGTGGACAAATTTATTAATAATGGGAGAAATTTTGTGAT 414
 DB 103 -----AspAlaAspProTrpLysAlaPheMetAlaGlnValGluValLeuIleAsp 119
 QY 415 ACACGGTTACAGAAAGCATAAAACAGCTAAAGTTTACAACTTTTAGAAGGATTTAGACAA 474
 DB 120 LysIleGluGluTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAsn 139
 QY 475 ATATTACAAAGCTATAATACAGCATATGATGGAGAAATTTAAAGACTACAGCT 534
 DB 140 AsnPheGluAspTyrValAsnAlaLeuAsnSerTrpLysLys----- 153
 QY 535 CCTGGATTACACCAATCATCAGCATTAACAACAGCTGCTTGAATCTTTAAATACGATTT 594
 DB 154 -----ThrProLeuSerLeuArgSerLysArgSerGlnAspArgIleArgGluLeuPhe 171
 QY 595 GAGAAATGTTCAAGATTTTATTTCGAGAAATACCTGGTTTCCAACTTTGAAACTTATAAA 654
 DB 172 SerGlnAlaGluSerHisPheArgAsnSerMetProSerPheAlaValSerLysPheGlu 191
 QY 655 ACGCTATTACCTATTATTCGCAAGCTCTAATTTTCAATTTTAAATTTATTATTAACAACAA 714
 DB 192 ValLeuPheLeuProThrTyrAlaGlnAlaAlaAsnThrHisLeuLeuLeuLysAsp 211
 QY 715 GGTGCTGAATGGCTGATGAATGGAATGCAGATATACATCTTCCAAATTTGAACTAAT 774
 DB 212 AlaGlnValPheGlyGluGluTrpGlyTyrSer-----Ser 223
 QY 775 GCTGGAACATCAGATGACTATATAAACTTTTAAAGAAATAATATACCTTAATATAGTAAC 834
 DB 224 GluAspValAlaGluPheTyrHisArgGlnLeuLysLeuThr---GlnGlnTyrThrAsp 242
 QY 835 TATTGTGCNAATACCTATAGAGAGGACTAATAAATCTTCGAAACGAACCTAATATGAGA 894
 DB 243 HisCysValAsnTrpTyrAsnValGlyLeuAsnGlyLeuArgGlySerThrTyrAspAla 262
 QY 895 TGGAGTATATTAATGAATATCGAAGATATATGACTATATTACTGTTATTAGATATATCGCT 954

DB 263 TrpValLysPheAsnArgPheArgArgGluMetThrLeuThrValLeuAspLeuIleVal 282
 QY 955 CAATTTTCTTTTATGATATAAAGAGATACAAAGATTCAATAGGAAGAAATAGGTGGCAATT 1014
 DB 283 LeuPheProPheTyrAspIleArgLeuTyrSerLys-----GlyVal 296
 QY 1015 AAACTCAACTTACAGAGAAATTTATACAACTGAAATAAATTTTGACCGCTCTTACTTAC 1074
 DB 297 LysThrGluLeuThrArgAspIlePheThrAspProIle---PheSerLeuAsnThrLeu 315
 QY 1075 CTTGAAATTCACCCCAATCTCGCTATATGGAATATATAATTAACACGCTTCAGGCGCTTAGA 1134
 DB 316 GlnGluTyrGlyProThrPheLeuSerIleGluAsnSerIleArgLysPro-----His 333
 QY 1135 TTATTTTCTTTTATGAGAACTTATATTTATACAAAA----- 1173
 DB 334 LeuPheAspTyrLeuGlnGlyIleGluPheHisThrArgLeuGlnProGlyTyrPheGly 353
 QY 1174 -----AATGAAACGTACGGAATCGTTAGTTGGTATTGCGAATCGTAATAGA 1221
 DB 354 LysAspSerPheAsnTyrTrpSerGlyAsnTyr-----ValGluThrArgProSer 370
 QY 1222 TCTACTTATGTCACGACGAACTGAAATATATATATGAGAAAGAAACAGGTCACCCACA 1281
 DB 371 IleGlySerSerLysThrIleThrSerProPheTyrGlyAspLysSerThrGluProVal 390
 QY 1282 AAAAACTTTAATACATTTGAATCCTATAAAGTTTCAATTTGTAAGTATAGTACAGTA 1341
 DB 391 GlnLys-----LeuSerPheAspGlyGlnLysValTyr-----ArgThrIle 404
 QY 1342 -----ACTCCTACTCCCCCTTTTCTTAAC-----ATATACCTTTTACAAATTAACAATT 1389
 DB 405 AlaAsnThrAspValAlaAlaTrpProAsnGlyLysValTyrLeuGlyValThrLysVal 424
 QY 1390 GAATCTTTATTAATAATTCACCTAGTAGTAATAATA-----ACATATTCAGCT--- 1437
 DB 425 AspPheSerGlnTyrAspAspGlnLysAsnGluThrSerThrGlnThrTyrAspSerLys 444
 QY 1438 -----GGGGGGAATTTATCTAATGATAAAAAACAACTGATTTTCAATTTCTGTGTA 1491
 DB 445 ArgAsnAsnGlyHisValSerAlaGlnAspSerIleAsp-----GlnLeuProGlu 462
 QY 1492 AAAGACTGTAACCAATTTATTAATCCAAATTTGTTACCAAGCTATATAGTATTAGTCAT 1551
 DB 463 ThrThrAspGluProLeu-----GluLysAlaTyrSerHis 474
 QY 1552 ATTTTATCCCGATTTTCTTTTATTAATTTATCTCTATAAAATTTGATTTAGCGCTAAATATA 1611
 DB 475 GlnLeuAsnTyrAlaGluCysPheLeuMetGlnAspArgArgGlyThrIle-----Pro 492
 QY 1612 TTATATACAGGTGATGATGAGACACAGATGATGTTTAAATAGAAATAATGCAATATCA 1671
 DB 493 PhePheThr-----TrpThrHisArgSerValAspPhePheAsnThrIleAsp 508
 QY 1672 GATAAATAATTAATCAATGATCCAGCAATCAAGGTAAACAGTCTTGATACAACTCTAAG 1731
 DB 509 AlaGluLysIleThrGlnLeuProValValLysAlaTyrAlaLeuSerSerGlyAlaSer 528
 QY 1732 GTAATTCAGGACCTGCTCATACAGGAGAACTTGGTTTATTTATCAAA----- 1779
 DB 529 IleIleGluGlyProGlyPheThrGlyAsnLeuLeuPheLeuLysGluSerSerAsn 548
 QY 1780 AGTCAAGGGGTTTAGAGATTACATGATAGAACTCTCTAATTTCTCAACAATCTTATACATT 1839
 DB 549 SerIleAlaLysPheLysValThrLeuAsnSerAlaAlaLeuLeuGlnArgTyrArgVal 568
 QY 1840 AGCTTCGATACGCTACAAATGGTGGAAATACTCTCTCTAATATATCTCTTACATA 1899
 DB 569 ArgIleArgTyrAlaSerThr-----ThrAsnLeuArgLeuPheVal 582
 QY 1900 CCAGGAGTAATAGGAATACCACTCCAGCTCAACGACTCAACAACTTTTCTGTTACAAATAT 1959


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QY 1330 GATGACAGTAAGTAACTCTACTCCCTCTTCTCTAATATATCTTATCAATTAATCAAA--- 1386
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Db 418 AspAsnLeuLeuPheAsnProPheLeuLeuGlyAspIleTyr---ThrIleAsnThrGly 436
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QY 1387 ATTGAACCTTTATTAAATAAT-----TCACCT 1413
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Db 437 TyrValSerTyrLeuAlaAsnLeuPheGlyIleTyrSerAlaAArgPheThrThrThrArg 456
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QY 1414 AGTAATAAATTAACATATTACCTGGGGGAATTTATCTATGATATAAAAAAACACTGAT 1473
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   |||
Db 457 SerIleGluLeuLeuTyr-----GluAsnGlnAArgValPheProAla 470
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QY 1474 TTTCAATTTCTGTAAAAAGAGACTGTAAACCAATTTATTAATCCAAATGTTTACCAGC 1533
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   |||
Db 471 TyrAsnHisGlnIleAArgGlu-----LeuProGly 480
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QY 1534 TATAATAGT-----TATAGTCATATTTTATCCAGCTTTTCTTTA 1572
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   |||
Db 481 ValAsnSerAspArgProThrAlaAlaAspTyrSerHisAArgLeuSerTyrIleSer--- 499
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   |||
QY 1573 TTTAATTTATCTATAAAATGGATTAGGCTAAGTAAATATATATATACAGGTGCATTA--- 1629
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   |||
Db 500 -----GlyPheAlaThrAspValGlyIleThrValLeuValTyr 512
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QY 1630 GGATCGACACACAGTAGTGTAAATAGAAATATGCAATATCA---GATAAAATATATACA 1686
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   |||
Db 513 GlyIleThrThrSerThrAlaAlaThrArgGluAsnAsnIleThrLeuAspAspArgIleVal 532
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QY 1687 ATGATCCAGCAATCAAAAGGTAAACAGTCTTGATACAAACTCTAAGGTAAATTCGAAGGACCT 1746
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   |||
Db 533 GlnLeuProAlaValLysGlyThrSerLeuAsn---AsnCysGlnValValAArgGlyThr 551
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   |||
QY 1747 GGTCTATACAGAGGAACCTGGTTTATTTATCAAGTCAAGGCGTGTAGAGATACATGT 1806
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   |||
Db 552 GlyPheThrGlyIleAspTrpLeuLysProAsnAsnAsnGlyThrPheSerLeuAlaLeu 571
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   |||
QY 1807 AGNACTCCTAAATTCACAACTCTTATACATTTAGACTTCGATCGCTACAAATGGTGCT 1866
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   |||
Db 572 GlyPhe---ArgSerThrTyrThrTyrArgLeuArgIleAArgTyrAlaAlaAlaGly 590
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QY 1867 GGAATACTCTTCCTTAATATCTCTTACAAATCACCAGGAGTAATAGGAATACCACTCAAA 1926
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   |||
Db 591 GlySer-----GlyPheSerLeuValIleSerAspGlnTyrGlyGluPhePro--- 606
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QY 1927 CGACTCAACAACACTTTTCTGGTACAAATATTAAT-----AATTTACAATACGGA 1977
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   |||
Db 607 ThrThrThrValSerLeuSerSerThrMetTyrSerLeuProGlnAsnValProTyrGlu 626
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QY 1978 GATTTGGGTATTTCCAAATTTCCAGTACAGTAACATTA----- 2016
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   |||
Db 627 AlaPheLysIleValAspLeuProSerThrValThrIleAArgAsnThrSerProAlaSer 646
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QY 2017 ---CCTTTAAATCGAAACATACCAATTTATATTTAATCGTGAGATGTATCAAAATTCAT 2073
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Db 647 ThrThrPheAArgLeuAspPheAArgPheIleValProLeuGlyIleLeuAlaAsn----- 664
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QY 2074 TTAATCATTTGATAAAATTTGAATTTATACCAATTTACTCTCTCTGTACGCCAAAATAGAGAA 2133
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Db 665 IleLeuIleAspArgIleGluPheValProIleGluGlySerLeuPheGluThr 684
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QY 2134 AAACAAAATTTAGAACTATCCAAACAAAATATAATATATTTTTCACAAATCATCAAAA 2193
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Db 685 LysGlnGlnLeuGluLysAlaAArgLysAlaValAsnHisLeuPheThrAspGlySerLys 704
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QY 2194 AATACTTTAAATATAGAACCCCAAACTATGATATTTGAT 2232
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Db 705 LysAlaLeuLysGluGlyThrThrAspTyrGluIleAsp 717
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RESULT 9

US-11-192-801-8

; Sequence 8, Application US/11192801

; Publication No. US20050273882A1

; GENERAL INFORMATION:

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; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/11/192,801
; PRIOR FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/10/232,665
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: non-naturally
; OTHER INFORMATION: occurring amino acid sequence encoded by SEQ ID NO:7
; FEATURE:
; NAME/KEY: PRT
; LOCATION: (1)..(653)
; OTHER INFORMATION: amino acid sequence for Cry3Bb variant v11231 encoded by SEQ ID NO
US-11-192-801-8
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Alignment Scores:
Pred. No.: 2,63e-45 Length: 653
Score: 683.00 Matches: 207
Percent Similarity: 44.58% Conservative: 122
Best Local Similarity: 28.05% Mismatches: 283
Query Match: 17.34% Indels: 126
DB: 7 Gaps: 28
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US-10-782-570-1 (1-2235) x US-11-192-801-8 (1-653)

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Db 3 AsnProAsnAsnArgSerGluHisAspThrIle-----LysValThrProAsnSer 19
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   |||
QY 64 AACAGAAATATGATCATCTTAGATACCTTACACAAATATCAAAATATCAACCAATTCACAA 123
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Db 20 GluLeuGlnThrAsnHisAsnGlnTyrProLeuAlaAspAsnProAsnSerThrLeuGlu 39
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   |||
QY 124 AACACAAATTTACAAAGAGTGGCTCAATATGTGTCAA---GGGAATACACAATATGGTGAT 180
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Db 40 GluLeuAsnTyrLysGluPheLeuAArgMetThrGluAspSerSerThrGluValLeuAsp 59
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QY 181 AATTTTCGAGACATTTGCTAGTGTGATACAAATTTGCT---GCAGTTAGTCGAGGTACTATT 237
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Db 60 Asn-----SerThrValLysAspAlaValGlyThrGlyIleSer 72
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QY 238 GTATCCGGTACTCTGTTAGCCGTATAGTGGGTCTACTTCTATATCCGACCGATAGGA 297
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Db 73 ValValGlyGlnIleLeuGlyValValGly-----ValPro 84
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QY 298 ATAATAGGTCTATAATAATATCTTTTGGTACCTTAATCACTGCTCTTTTTCGCGCGGGA 357
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   |||
Db 85 PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnThrIleTrpProSer--- 103
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QY 358 GAACAACAGCAAAAACAGTATGACACAAATTTATTAATGGAGAAATTTTGTGTGATACA 417
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Db 104 -----AspAlaAspProTrpLysAlaPheMetAlaGlnValGluValLeuAspLys 121
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QY 418 CCCTTAACAGAAAGCATATAAACAGCTTAAAGCTTAAACACTTTAGAGAGATTTAGACAATA 477
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Db 122 LysIleGluGluTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAsnAsn 141
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QY 478 TTACAAAGCTATAATACAGCATTAGATGATTGGAGAAATTTAAAGACTACAGCTCCT 537
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Db 142 PheGluAspTyrValAsnAlaLeuAsnSerTrpLysLys----- 154
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QY 538 GGATTACCACCATCATCAGCATTTACACAAAGCTTCGCTTGACTCTTAAATACGATTTGAG 597
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Db 155 ---ThrProLeuSerLeuAArgSerLysAArgSerGlnAspArgIleAArgGluLeuPheSer 173
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QY 1546 AGTCATATTTATCCAGCTTTTCTTTATTTATTTATTCCTATAAAATGGGATTAGCGCTA 1605
Db      :::::
QY 474 SerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGlnAspArgArgGlyThrIle--- 492
QY 1606 AATATATATATACAGGTGCATTAGGATGGACACACAGTAGTGTATTAATAAGAAATAATGCA 1665
Db      :::::
QY 493 --ProPhePheThr-----TrpThrHisArgSerValAspPheAsnThr 507
QY 1666 ATATCAGATAAATAATTACATGATCCAGCAATCAAGGTAAACAGTCTTGATACAAAC 1725
Db      :::::
QY 508 IleAspAlaGluLysIleThrGlnLeuProValValLysAlaTyrAlaLeuSerSerGly 527
QY 1726 TCTAAGGTAAATTGAAGGACCTGGTCATACAGGAGGAACTTGGTTTATTATACAA----- 1779
Db      :::::
QY 528 AlaSerIleIleGluGlyProGlyPheThrGlyAsnLeuLeuPheLeuLysGluSer 547
QY 1780 -----AGTCAAGGCGCTTATAGAGATTACATGTAGAACTCCTAAATTCACACAATCTTAT 1833
Db      :::::
QY 548 SerAsnSerIleAlaLysPheLysValThrLeuAsnSerAlaAlaLeuLeuGlnArgTyr 567
QY 1834 TACATTAGACTTCGATAGCTACAAATGGTCTCGGAATATCTCTTCTTAATATCTCTT 1893
Db      :::::
QY 568 ArgValArgIleArgTyrAlaSerThr-----ThrAsnLeuArgLeu 581
QY 1894 ACAATACCAGGAGTAATAGGAATACCACTCAACGACTCAACACACTTTTCTCGGTACA 1953
Db      :::::
QY 582 PheVal-----GlnAsnSerAsnAsnAspPheLeuValIle 593
QY 1954 AATTATATAT-----AATTACAAATACGGAGATTTTGGGTATTTTC 1992
Db      :::::
QY 594 TyrIleAsnLysThrMetAsnLysAspAspLeuThrTyrGlnThrPheAspLeuAla 613
QY 1993 CAATTCACAGTACAGTAAACATTACCTTTAAATCGAACATACCAATTTATATTAATCGT 2052
Db      :::::
QY 614 ThrThrAsnSerAsnMetGlyPheSerGlyAspLysAsnGluLeuIleGlyAlaGlu 633
QY 2053 CGAGATGTATCAATTCATTTAATCATTCATATAAAATTTGAATTTATACCAAT 2106
Db      :::::
QY 634 SerPheValSerAsnGluLysIleTyrIleAspLysIleGluPheIleProVal 651

RESULT 12
US-11-192-801-14
; Sequence 14, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/11/192,801
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/10/232,665
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide encoded by SEQ ID NO:
; NAME/KEY: PRT
; LOCATION: (1)..(653)
; OTHER INFORMATION: Cry3BB1 variant v11231
US-11-192-801-14
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Alignment Scores:
Pred. No.: 2,63e-45 Length: 653
Score: 683.00 Matches: 207
Percent Similarity: 44.58% Conservative: 122
Best Local Similarity: 28.05% Mismatches: 283
Query Match: 17.34% Indels: 126
DB: 7 Gaps: 28

US-10-782-570-1 (1-2235) x US-11-192-801-14 (1-653)
QY 4 AATCAAAATAATAATGAATATGAGATTATCGATTATCAAAAGAAATTTATCTTATCTCTTCT 63
Db      :::::
QY 3 AsnProAsnAsnArgSerGluHisAspThrIle-----LysValThrProAsnSer 19
QY 64 AACAGAAATATGATCATCTTAGATACCTTTACACAATATCCAAATATCCAAATCAACCAATTA 123
Db      :::::
QY 20 GluLeuGlnThrAsnHisAsnGlnTyrProLeuAlaAspAsnProAsnSerThrLeuGlu 39
QY 124 AACACAAATTACAAGAGTGGCTCAATATGTGTCAA---GGGAATACACAATATGGTGAT 180
Db      :::::
QY 40 GluLeuAsnTyrLysGluPheLeuArgMetThrGluAspSerThrGluValLeuAsp 59
QY 181 AATTTCCGAGACATTTGCTAGTGTCTGATACAATTTGCT---GCAGTTAGTCGAGGTACTATT 237
Db      :::::
QY 60 Asn-----SerThrValLysAspAlaValGlyThrGlyIleSer 72
QY 238 GTATCCGGTACTCTGTAGCGGTATATAGTGGGTCTACTTCTATATCCGGACCGATAGGA 297
Db      :::::
QY 73 ValValGlyGlnIleLeuGlyValValGly-----ValPro 84
QY 298 ATAATAGTGTCTATAATAATATCTTTTGGTACCTTAATCACTGTCTTTTGGCCCGCGGA 357
Db      :::::
QY 85 PheAlaGluAlaLeuThrSerPheTyrGlnSerPheLeuAsnThrIleTrpProSer--- 103
QY 358 GAACACAGACAAAACAGTATGGACACAAATTTATTAATAATGGAGAAATTTTGTGTGATACA 417
Db      :::::
QY 104 -----AspAlaAspProTrpLysAlaPheMetAlaGlnValGluValLeuIleAspLys 121
QY 418 CCGTTAACAGAAAGCATAAACAGCTAAAGTTACAACTTTAGAGAGATTTAGACAATA 477
Db      :::::
QY 122 LysIleGluGluTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAsn 141
QY 478 TTACAAAGCTATAATACAGCATTAGATGATTGGAGAAATTTAAAAAGACTACAAGCTCCT 537
Db      :::::
QY 142 PheGluAspTyrValAsnAlaLeuAsnSerTrpLys----- 154
QY 538 GGATTACCCCATCATCAGCATTTACAACAGCTGCTTGACTCTTAAATAACGATTGAG 597
Db      :::::
QY 155 ---ThrProLeuSerLeuArgSerLysArgSerGlnAspArgIleArgGluLeuPheSer 173
QY 598 AATGTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCACTTGAACCTTATAAAGC 657
Db      :::::
QY 174 GlnAlaGluSerHisPheArgAsnSerMetProSerPheAlaValSerLysPheGluVal 193
QY 658 CTATTACTACTATTTATGCGCAAGCTGCTAAATTTTCATTTTAAATTTTATTAACAAGGT 717
Db      :::::
QY 194 LeuPheLeuProThrTyrAlaGlnAlaAsnThrHisLeuLeuLeuLeuLysAspAla 213
QY 718 GCTGAATTTGGCTGATGAATGGATGCAGATATACATCCTTCCAAATTTGAACCTTAATGCT 777
Db      :::::
QY 214 GlnValPheGlyGluGluTrpGlyTyr----- 222
QY 778 GGAACATCAGATGAC-----TATATTAACCTTTTAAAAAGAAATATACCTAAATAT 828
Db      :::::
QY 223 ---SerSerGluAspValAlaGluPheTyrArgGlnLeuLysLeuThrGlnGlnTyr 241
QY 829 AGTAACCTATTGTGCAAAATACCTATAGAGAGAGACTTAAATAAACTTCGAAACGAACCTAAT 888
Db      :::::
QY 242 ThrAspHisCysValAsnThrTrpTyrAsnValGlyLeuAsnGlyLeuArgGlySerThrTyr 261
QY 889 ATGAGATGGAGTATATTTAATGATTTATCGAAGATATATGACTATTACTGTATTAGATACT 948
Db      :::::
QY 262 AspAlaTrpValLysPheAsnArgPheArgGluMetThrLeuThrValLeuAspLeu 281
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OTHER INFORMATION: CRY3BB1 variant 11231mw1
US-11-192-801-18

Alignment Scores:

Pred. No.:	2,63e-45	Length:	653
Score:	683.00	Matches:	207
Percent Similarity:	44.58%	Conservative:	122
Best Local Similarity:	28.05%	Mismatches:	283
Query Match:	17.34%	Indels:	126
	7	Gaps:	28

US-10-782-570-1 (1-2235) x US-11-192-801-18 (1-653)

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QY 4 AATCAAAATAATAATAAGTATATGAGATTTCGATTCAAAGAAATTTATCTTCTCTCT 63
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3 AenProAsnAsnArgSerGluHisaspThrle-----LysValThrProAsnSer 19
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 64 AACAGAAATATTGATCATTTCTAGATACCTTACACAAATAATCAAAATCAACCAATACAA 123
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 20 GluLeuGlnThrAsnHisAsnGlnTyrProLeuAlaAspAsnProAsnSerThrLeuGlu 39
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 124 AACCAAAATACAAAGAGTGGCTCAATATGTCTCAA---GGGAATACACAATATGGTGAT 180
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 40 GluLeuAsnTyrLysGluPheLeuArgMetThrGluAspSerSerThrGluValLeuAsp 59
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 AATTTTCGAGACATTTGCTAGTCTGATACAAATGTCT---GCAGTTAGTGCAGGTACTATT 237
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 60 Aen-----SerThrValLysAspAlaValGlyThrGlyLeuSer 72
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 238 GTATCCGGTACTCTGTAGCCGGTATAGTGGGCTCACTTCTATATCCGACCGATAGGA 297
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 73 ValValGlyGlnLeuGlyValValGly-----ValPro 84
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 238 ATAATAGTGCTATTAATTAATATCTTTTGGTACCCTAATCACTGTCTTTGGCCCGGGA 357
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 85 PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnThrIleTrpProSer--- 103
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 358 GAACAAGCAAAACAGTAGTGACACAAATTTATAAATGGGAGAAATTTTGTTCATACA 417
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 104 -----AspAlaAspProTrpLysAlaPheMetAlaGlnValGluLeuGlnAsnLys 121
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 418 CCGTTAACAGAAAGCATAAACAGCTAAAGTTTACAACTTTTGAAGAGGATTTAGACAAATA 477
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 122 LysIleGluGluTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAsnAsn 141
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 478 TTCAAAGCTAATAATACAGCATAGATGATGGAGAAATTAATAAAGACTACAAGCTCCT 537
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 142 PheGluAspTyrValAsnAlaLeuAsnSerTrpLysLys----- 154
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 538 GGATTCACCATCATCAGCATTAACAACAGCTGCTTGAATCTTAAATAACGATTGAG 597
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 155 ----ThrProLeuSerLeuArgSerLysArgSerGlnGlyArgIleArgGluLeuPheSer 173
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 598 AATGTTCAATGATTTTATTCGAGAAATPACTGGTTTCCAACTTGAACCTTATAAAACG 657
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 174 GlnAlaGluSerHisPheArgAsnSerMetProSerPheAlaValSerLysPheGluVal 193
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 658 CTATTACTACCTATTATTCGCAAGCTGCTAATTTTCATTAAATTTTATTACACAAGGT 717
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 194 LeuPheLeuProThrTyrAlaGlnAlaAlaAsnThrHisLeuLeuLeuLysAspAla 213
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 718 GCTGAATGCTGATGAATGAATGATGATACATACCTCTTCAAAATGAACCTAATGCT 777
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 214 GlnValPheGlyGluGlnTrpGlyTyr----- 222
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 778 GGAAATCATGATGAC-----TATTATAAATCTTTTAAAGAAATAATACCTAAATAT 828
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 223 ---SerSerGluAspValAlaGluPheTyrArgGlnLeuLysLeuThrGlnGlnTyr 241
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 829 AGTAACATATTGTGCAATACCTATTAGAGAAGGACTAAATAAATCTCGAAACGAACTAAT 888
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 242 ThrAspHisCysValAsnTrpTyrAsnValGlyLeuAsnGlyLeuArgGlySerThrTyr 261
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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QY 889 ATGAGATGGAGTATATTTAATGATTAATCGAAGATATATGACTATTACTGTATTAGATACT 948
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 262 AspAlaTrpValLysPheAsnArgPheArgArgGluMetThrLeuThrValLeuAspLeu 281
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 949 ATCGCTCAATTTCTTTTATGATATAAAGAGATACAAAGATTCATAGGAAGAATAGGT 1008
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 282 IleValLeuPheProPheTyrAspIleArgLeuTyrSerLys----- 295
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1009 GGCATTAAACCTGAACCTTACAAAGAGAAATTTATACAACTGAAATATAATTTTGACCGCTCT 1068
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 296 GlyValLysThrGluLeuThrArgAspIlePheThrAspProIle---PheLeuLeuThr 314
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1069 ACTTACCTTGAAATTCACCCCAATCTCGCTAATATGGAATATAATTTAAACCGTTCAGGG 1128
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 315 ThrLeuGlnLysTyrGlyProThrPheLeuSerIleGluAsnSerIleArgLysPro--- 333
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1129 CTTAGATTATTTTCAATTTTATAGTGAATCTTATATTTATATACAAA----- 1173
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 334 --HisLeuPheAspTyrLeuGlnGlyIleGluPheHisThrArgLeuArgProGlyTyr 352
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1174 -----AATGAAACGTACCGGAATCGTTTGTAGTTGGTATTGCGAATCGT 1215
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 353 PheGlyLysAspSerPheAsnTyrTrpSerGlyAsnTyr-----ValGluThrArg 369
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1216 AATAGATCTACTTATGCTACGACGAGAACTGAAATTTATATATGGAGAAGAACAGGTCCA 1275
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 370 ProSerIleGlySerSerLysThrIleThrSerProPheTyrGlyAspLysSerThrGlu 389
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1276 CCCAACAAACAACTTTAATACCAATTTGAATCCCTATAAAGTTTCAATTTGTAACGTAGA 1335
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 390 ProValGlnLys-----LeuSerPheAspGlyGlnLysValTyr-----Arg 403
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1336 CAAGTA-----ACTCCTACTTCCCTTTCCTAAC-----ATATACCTTTCAATTAAT 1383
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 404 ThrIleAlaAsnThrAspValAlaAlaTrpProAsnGlyLysValTyrLeuGlyValThr 423
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1384 CAATTTGAATCTTTTAAATAAATTCACCTAGTATAATAATTA-----ACATATTCA 1434
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 424 LysValAspPheSerGlnTyrAspAspGlnLysAsnGluThrSerThrGlnThrTyrAsp 443
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1435 GCT-----GGGGGAATTTATCTAATGATAAATAAACAACCTGATTTTCAATTTCT 1485
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 444 SerLysArgAsnAsnGlyHisValSerAlaGlnAspSerIleAsp-----GlnLeuPro 461
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1486 GTAAAAAAGACTGTAAACCAATTTAATCCAAATTTGTTTACCAAGCTATAATAGTTAT 1545
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 462 ProGluThrThrAspGluProLeu-----GluLysAlaTyr 473
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1546 AGTCATATTTTATCCAGTTTCTTTTATTTAATTTCTTATATAAATTTGGATTAGCGCTA 1605
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 474 SerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGlnAspArgArgGlyThrIle--- 492
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1606 AATATATTATATACAGGTGCATTAGATGGACACACAGTAGTGTTAATAGAAATATGCA 1665
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 493 ---ProPhePheThr-----TrpThrHisArgSerValAspPhePheAsnThr 507
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1666 ATATCAGATAAAATAATTTACATGATCCAGCAATCAAAGGTAAACAGTCTTCATACAAAC 1725
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 508 IleAspAlaGluLysIleThrGlnLeuProValValLysAlaTyrAlaLeuSerSerGly 527
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1726 TCTAAGTAAATTTGAAGGACCTGGTGCATACAGAGAGAACTTGGTTTATTATACAA----- 1779
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 528 AlaSerIleIleGluGlyProGlyPheThrGlyGlyAsnLeuLeuPheLeuLysGluSer 547
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1780 -----AGTCAAGGGCGTTTAGAATTTAGATTCATGAGACTCTTAATTTCTACACAATCTTAT 1833
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 548 SerAsnSerIleAlaLysPheLysValThrLeuAsnSerAlaAlaLeuLeuGlnArgTyr 567
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1834 TACATTAGACTTCGTAGTACCTACAAATGGTGTGCGAAATATCTCTCTTAATATATCTCT 1893
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 568 ArgValArgIleArgTyrAlaSerThr-----ThrAsnLeuArgLeu 581
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1894 ACAATACCGAGGAGTAGTAATAGGAATACCACTCAACGACTCAACACACTTTTCTGCTGACA 1953
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db      582 PheVal-----GlnSerAsnAsnAspPheLeuValIle 593
Qy      1954 AATTATAAT-----AATTACAATACGGAGATTTGGGTATTTC 1992
Db      594 TyrIleAsnLysThrMetAsnLysAspAspLeuThrTyrGlnThrPheAspLeuAla 613
Qy      1993 CAATTTCCAAGTACAGTACATTACCTTTAAATCGAAACATACCAATTTATATTAATCGT 2052
Db      614 ThrThrAsnSerAsnMetGlyPheSerGlyAspLysAsnGluLeuIleGlyAlaGlu 633
Qy      2053 GCAGATGTATCAAAATTTCAATTTTAAATCATGATAAAATTTGAATTTATACCAAT 2106
Db      634 SerPheValSerAsnGluLysIleTyrIleAspLysIleGluPheIleProVal 651

RESULT 15
US-11-192-801-20
; Sequence 20, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/11/192,801
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/10/232,665
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PRT
; LOCATION: (1)..(653)
; OTHER INFORMATION: Cry3Bb1 variant 11231mv1
US-11-192-801-20

Alignment Scores:
Pred. No.: 2,63e-45 Length: 653
Score: 683.00 Matches: 207
Percent Similarity: 44.58% Conservative: 122
Best Local Similarity: 28.05% Mismatches: 283
Query Match: 17.34% Indels: 126
DB: 7 Gaps: 28

US-10-782-570-1 (1-2235) x US-11-192-801-20 (1-653)
Qy      4 AATCAAAATATATATGAATATGAGATTATCGAATTCAAGAAATTTATCTTATCTCTCT 63
Db      3 AsnProAsnAsnArgSerGluHisAspThrIle-----LysValThrProAsnSer 19
Qy      64 AACGAAATATGTATCTTCTAGTACCCCTTACACAAATATCCAAATCAACCAATTACAA 123
Db      20 GluLeuGlnThrAsnHisAsnGlnTyrProLeuAlaAspAsnProAsnSerThrLeuGlu 39
Qy      124 AACCAAAATTAACAAGAGTGGCTCAATATGTGTCAA---GGGAATACACATATGTGTAT 180
Db      40 GluLeuAsnTyrLysGluPheLeuArgMetThrGluAspSerSerThrGluValLeuAsp 59
Qy      181 AATTTCGAGACATTTGCTAGTCTGCTGATACAAATTCGT---GCAGTTAGTGCAGGTACTATT 237
Db      60 Asn-----SerThrValLysAspAlaValGlyThrGlyIleSer 72
Qy      238 GTATCCGGTACTCTGTAGCCGGTATAGTGGGCTCACTTCTATATCCGGACCATAGGA 297
Db      73 ValValGlyGlnIleLeuGlyValValGly-----ValPro 84
Qy      298 ATAATAGTGTCTATAATAATATCTTTTGGTACCCTCAATCACTGTCTTTTGGCCCGCGGA 357

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Db      85 PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnThrIleTyrProSer--- 103
Qy      358 GAACAGACAAAAACAGTATCGACACAATTTATTAAATGGGAGAAATTTTGTGTGATACA 417
Db      104 -----AspAlaAspProTyrLysAlaPheMetAlaGlnValGluValLeuIleAspLys 121
Qy      418 CCGTTAACAGAAACATAAAACAGCTAAAGTTACAACTTTAGAGAGATTTAGACAAATA 477
Db      122 LysIleGluGluTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAsnAsn 141
Qy      478 TTACAAAGCTATATAATCAGCATTTAGATGATTGGAGAAAAATTTAAAAAGACTACAAGCTCCT 537
Db      142 PheGluAspTyrValAsnAlaLeuAsnSerTyrLysLys----- 154
Qy      538 GGATTACCATCATCATCAGCATTTACAACAGCTGCTTGTGACTCTTAAATAACGATTTGAG 597
Db      155 ---ThrProLeuSerLeuArgSerLysArgSerGlnGlyArgIleArgGluLeuPheSer 173
Qy      598 AATGTTCCACAATGATTTTATTTCGAGAAATACCTGGTTTCCAACTTGAACCTTATAAAACG 657
Db      174 GlnAlaGluSerHisPheArgAsnSerMetProSerPheAlaValSerLysPheGluVal 193
Qy      658 CTATTACTACTATTATATGCGCAAGCTGCTAAATTTTCATTTAAATTTTATTACAAACAGGT 717
Db      194 LeuPheLeuProThrTyrAlaGlnAlaAsnThrHisLeuLeuLeuLeuLysAspAla 213
Qy      718 GCTGAATGCTGATGAATGCAATGCAGATATATACCTCTTCACAAATTTGAACCTTAATGCT 777
Db      214 GlnValPheGlyGluGluTyrGlyTyr----- 222
Qy      778 GGAACATCAGATGAC-----TATTATAAACTTTTAAAGAAATATATACCTAAATAT 828
Db      223 ---SerSerGluAspValAlaGluPheTyrArgArgGlnLeuLysLeuThrGlnGlnTyr 241
Qy      829 AGTAACTATTGTGCAATACCTATAGAGAGAGAGCTAAATAAACTTCGAAACGAACTAAAT 888
Db      242 ThrAspHisCysValAsnTyrTyrAsnValGlyLeuAsnGlyLeuArgGlySerThrTyr 261
Qy      889 ATGAGATGGAGTATATTAAATGATTATCGAAGATATATGACTATTACTGTATTAGTACT 948
Db      262 AspAlaTyrValLysPheAsnArgPheArgGluMetThrLeuThrValLeuAspLeu 281
Qy      949 ATCGCTCAATTTCTTTTATATATAAAGAGATACAAAGATCAATAGGAAGAAATAGGT 1008
Db      282 IleValLeuPheProPheTyrAspIleArgLeuTyrSerLys----- 295
Qy      1009 GGCAATTAAAACTGAACCTTACAGAGAAATTTATACAACTGAAATATAATTTTGACCGCTT 1068
Db      296 GlyValLysThrGluLeuThrArgAspIlePheThrAspProIle---PheLeuLeuThr 314
Qy      1069 ACTTACCTTGAATTCACCCCAATCTCGCTATATATGAATATATATTTAACACGTTCAAGG 1128
Db      315 ThrLeuGlnLysTyrGlyProThrPheLeuSerIleGluAsnSerIleArgLysPro--- 333
Qy      1129 CTTAGATTATTTTCATTTTGTAGATGAATTTATATTTTATACAAA----- 1173
Db      334 ---HisLeuPheAspTyrLeuGlnGlyIleGluPheHisThrArgLeuArgProGlyTyr 352
Qy      1174 -----AATGAAACGTCAGGGAATCGTTTAGTTGTATTTCGAAATCGT 1215
Db      353 PheGlyLysAspSerPheAsnTyrTyrSerGlyAsnTyr-----ValGluThrArg 369
Qy      1216 AATAGATCTACTTATGCTACGACAGGAACCTGAAATTTATATATGAGAGAAACAGGTTCCA 1275
Db      370 ProSerIleGlySerSerLysThrIleThrSerProPheTyrGlyAspLysSerThrGlu 389
Qy      1276 CCACACAAACAACTTTAATACCATTTGAATCTCTATAAACTTCAATTTGTAACGTATAGA 1335
Db      390 ProValGlnLys-----LeuSerPheAspGlyGlnLysValTyr-----Arg 403
Qy      1336 CAAGTA-----ACTCTACTCTCCCTTTTCTTAAC-----ATATACTTTTACAATTAAT 1383
Db      404 ThrIleAlaAsnThrAspValAlaAlaTyrProAsnGlyLysValTyrLeuGlyValThr 423

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 12, 2006, 06:18:19 ; Search time 43 Seconds
(without alignments)
8594.425 Million cell updates/sec

Title: US-10-782-570-1

Perfect score: 3939

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-USER=US10782570@cgn_1_1_50@runat_12012006_060222_7551 -NCPU=6 -ICPU=3
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:

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- 3: /cgn2_6/ptodata/1/1aa/H COMB.pep.*
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- 5: /cgn2_6/ptodata/1/1aa/RE COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1153	29.3	1180	4	PCT-US94-07902-28
3	900	22.8	686	2	US-09-224-024-31
4	900	22.8	686	4	PCT-US94-07902-31
5	787.5	20.0	1169	1	US-08-315-468-4
6	706	17.9	651	1	US-08-315-468-6
7	706	17.9	651	2	US-07-941-650A-4
8	706	17.9	659	2	US-08-996-441B-112
9	706	17.9	659	2	US-08-993-722A-112
10	706	17.9	659	2	US-08-993-170A-112
11	706	17.9	659	2	US-08-993-775B-112
12	706	17.9	659	2	US-09-427-770-112

13	706	17.9	659	2	US-09-427-769-112	Sequence 112, App
14	700	17.8	652	2	US-08-996-441B-110	Sequence 110, App
15	700	17.8	652	2	US-08-993-722A-110	Sequence 110, App
16	700	17.8	652	2	US-08-993-170A-110	Sequence 110, App
17	700	17.8	652	2	US-08-993-775B-110	Sequence 110, App
18	700	17.8	652	2	US-09-377-466B-4	Sequence 4, Appli
19	700	17.8	652	2	US-09-427-770-110	Sequence 110, App
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21	700	17.8	652	2	US-10-232-665-4	Sequence 4, Appli
22	700	17.8	652	4	PCT-US92-00040-2	Sequence 2, Appli
23	693	17.6	652	2	US-09-377-466B-6	Sequence 6, Appli
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25	691	17.5	652	2	US-08-996-441B-4	Sequence 4, Appli
26	691	17.5	652	2	US-08-996-441B-10	Sequence 10, Appl
27	691	17.5	652	2	US-08-996-441B-28	Sequence 28, Appl
28	691	17.5	652	2	US-08-996-441B-44	Sequence 44, Appl
29	691	17.5	652	2	US-08-996-441B-68	Sequence 68, Appl
30	691	17.5	652	2	US-08-996-441B-98	Sequence 98, Appl
31	691	17.5	652	2	US-08-996-441B-111	Sequence 111, App
32	691	17.5	652	2	US-08-993-722A-4	Sequence 4, Appli
33	691	17.5	652	2	US-08-993-722A-10	Sequence 10, Appl
34	691	17.5	652	2	US-08-993-722A-28	Sequence 28, Appl
35	691	17.5	652	2	US-08-993-722A-44	Sequence 44, Appl
36	691	17.5	652	2	US-08-993-722A-68	Sequence 68, Appl
37	691	17.5	652	2	US-08-993-722A-98	Sequence 98, Appl
38	691	17.5	652	2	US-08-993-722A-111	Sequence 111, App
39	691	17.5	652	2	US-08-993-170A-4	Sequence 4, Appli
40	691	17.5	652	2	US-08-993-170A-10	Sequence 10, Appl
41	691	17.5	652	2	US-08-993-170A-28	Sequence 28, Appl
42	691	17.5	652	2	US-08-993-170A-44	Sequence 44, Appl
43	691	17.5	652	2	US-08-993-170A-68	Sequence 68, Appl
44	691	17.5	652	2	US-08-993-170A-98	Sequence 98, Appl
45	691	17.5	652	2	US-08-993-170A-111	Sequence 111, App

ALIGNMENTS

RESULT 1
US-09-224-024-28
; Sequence 28, Application US/09224024
; Patent No. 6056953
; GENERAL INFORMATION:
; APPLICANT: Jewel Payne
; TITLE OF INVENTION: Materials and Methods for the Control of
; CALLIPHORIDAE PESTS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESS: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,024
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,226
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA79
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800

Qy	943	GATACTATCGCTCAATTTCTTTTATGATATAAAGAGATACAAGAATTCATATAGGAAGA	1002
Db	305	AspLeuValalaLeuPheProAsnTyrAspValGlyLysTyrProIle-----	320
Qy	1003	ATAGGTGSCATTAACACTGAACTTACAGAGAAATTTATACACCTGAAATAAATTTTCAC	1062
Db	321	-----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal-----LeuAsnPheGlu	337
Qy	1063	CGTCTTACTACCTTGAATTCACCAACCAATCCGCTATATATGGAATATAATTTAAACACGT	1122
Db	338	GluSerProTyrLysTyrTyr-----AspPheGlnTyrGlnGluAspSerLeuThrArg	355
Qy	1123	TCAGGGCTTAGATTATTTTCATTTTATAGAACTTATATATTTTATACAAAATAATGAAACG	1182
Db	356	ArgPro---HisLeuPheThrTrpLeuAspSerLeuAsnPheTyrGluLysAlaGlnThr	374
Qy	1183	TACGGGAATCGTTAGTTGGTATTGCGAATCGTAAATAGACTACTATTATGCT-----	1233
Db	375	ThrProAsnAsnPhePhe-----ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn	393
Qy	1234	ACGACAGGAACGTGAATTTATATATGGAAGAAGACAGCTCCACCACCAACAAAACCTTTA	1293
Db	394	IleSerGlnLysSerSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu	413
Qy	1294	ATACCATTTGGAATCCTATAAAGTTTCAATTTGTAATCGATGACAGTAACCTCTACTTCC	1353
Db	414	-----GlyLeuAlaThrAsnIleTyrIlePheLeuLeuAsnValIleSerLeuAspAsn	431
Qy	1354	CCTTTTCTTAACATATCTTACAAATTAATCAAAATGCACTTTATTAATAATTCACCT	1413
Db	432	LysTyrLeuAsnAspTyrAsnAsnIleSerLysMetAspPhePheIleThrAsnGlyThr	451
Qy	1414	-----AGTAATAAATTAACATATTACGTGGGGGAATTTATCTAATGATAAAAAA	1464
Db	452	ArgLeuLeuGluLysGluLeuThr-----AlaGlySerGlyGlnIleThrTyrAspValAsn	470
Qy	1465	ACAACTGATTTTCAATTTCTCTGTAATAAAAAAGACTGTAAACCAATTTATTAATCCAAAT	1524
Db	471	LysAsnIlePheGlyLeuProIleLeuLysProArgGluAsnGlnAlaIleProThrLeu	490
Qy	1525	TTACCAAGCTATAATAGTATTAGTCATATTTTATCCAGTTTCTTTATTTAATTATAT	1581
Db	491	PheProThrTyrAspAsnTyrSerHisIleLeuSerPheIleLysSerLeuSerIlePro	510
Qy	1582	---TCCTATAAAATTTGGATTAGCGCTAAATATATATATACAGTGCATTTAGGATGACA	1638
Db	511	AlaThrTyrLys-----ThrGlnValTyrThrPheAla-----TrpThr	523
Qy	1639	CACAGTAGTGTTAATAGAAATAATGCAATATCAGATAAAATAATTAACAATGATCCAGCA	1698
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Qy	1599	ATCAAGGTAAACAGTCTTTGATACAACTCTAAGTAAATTCAGAGCACTGTGTCATACAGGA	1758
Db	544	ValLysAlaAsnSerLeuGlyThrAlaSerLysValValGlnGlyProGlyHisThrGly	563
Qy	1759	GGAACTTGGTTTATTTACAAGTCAGGGCGTTTACAGATTACATCTAGAACTCCCTAAT	1818
Db	564	GlyAspLeuIle-----AspPheLysAspHisPheLysIleThrCysGlnHisSerAsn	581
Qy	1819	TCTACACATCTTTATACATTAGACTTCGATACGCTACAAATGGTGTGGAAATACTCTT	1878
Db	582	PheGlnGlnSerTyrPheIleArgIleArgTyrAlaSerAsnGlySerAlaAsnThrArg	601
Qy	1879	CCTAATATATCTCTTACAAATCACGAGGATTAATAGGAATACCACTCAACGACTCAACAAC	1938
Db	602	AlaValIleAsnLeuSerIleProGlyValAlaGluLeu---GlyMetAlaLeuAsnPro	620
Qy	1939	ACTTTTTCTGTCAAAATTAATAATTTACATACCGAGATTTTGGTATTTTCCAAATTT	1998
Db	621	ThrPheSerGlyThrAspTyrThrAsnLeuLysTyrLysAspPheGlnTyrLeuGluPhe	640
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Db      641 SerAsnGluValIysPheAlaProAsnGlnAsnIleSerLeuValPheAsnArgSerAasp 660
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Qy      2059 GTA---TCAAATTCAAATTTTAATCATTGATATAAAATTGAATTTATACCAATTACTTCTCT 2115
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Db      661 ValTyrThrAsnThrThrValIleAspIleAspIleGluPheLeuProIleThrArgSer 680
      :|||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Qy      2116 GTACGCCAAATAGACAGAAAACAAAAATTAGAAACTATCCAAAACAAAAATAAATACATTT 2175
      :|||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db      681 IleArgGluAspArgGluIysGlnIysLeuGluThrValGlnGlnIleIleAsnThrPhe 700
      :|||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Qy      2176 TTCACAAATCATACAAAAATATCTTTAAATATATAGAACGCCACAAACTATGATATTGAT 2232
      ::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      701 TyrAlaAsnProIleIysAsnThrLeuGlnSerGluLeuThrAspTyrAspIleAasp 719
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RESULT 3
US-09-224-024-31
; Sequence 31, Application US/09224024
; Patent No. 6056953
; GENERAL INFORMATION:
; APPLICANT: Jewel Payne
; APPLICANT: Leslie Hickie
; TITLE OF INVENTION: Materials and Methods for the Control of
; TITLE OF INVENTION: Calliphoridae Pests
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,024
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,226
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA79
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 686 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-224-024-31

Alignment Scores:
Pred. No.: 3-25e-73 Length: 686
Score: 900.00 Matches: 251
Percent Similarity: 48.03% Conservative: 115
Best Local Similarity: 32.94% Mismatches: 268
Query Match: 22.85% Indels: 128
DB: 2 Gaps: 32

US-10-782-570-1 (1-2235) x US-09-224-024-31 (1-686)

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Db 655 AspTyrThrGluLeuAsnIleGluLeuThrGlnLysIleValAsnAspLeuPheVal 674
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RESULT 4
PCT-US94-07902-31
; Sequence 31, Application PC/TUS9407902
; GENERAL INFORMATION:
; APPLICANT: Street address: 4980 Carroll Canyon Road
; APPLICANT: City: San Diego
; APPLICANT: State/Province: California
; APPLICANT: Country: US
; APPLICANT: Postal code/Zip: 92121
; APPLICANT: Phone number: (619) 453-8030 Fax number: (619) 453-6991
; APPLICANT: Telex number:
; TITLE OF INVENTION: Materials and Methods for the Control of
; TITLE OF INVENTION: Calliphoridae Pests
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: PCT/US94/07902
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA79
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 686 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07902-31

Alignment Scores:
Pred. No.: 3,25e-73 Length: 686
Score: 900.00 Matches: 251
Percent Similarity: 48.03% Conservative: 115
Best Local Similarity: 32.94% Mismatches: 268
Query Match: 22.85% Indels: 128
DB: 4 Gaps: 32

US-10-782-570-1 (1-2235) x PCT-US94-07902-31 (1-686)

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Db 6 AsnLysAsnGluTyrGluIlePheAsnAlaProSerAsnGlyPheSerLysSerAsnAsn 25
QY 73 ATTGATCATCTTAGATACCTTACACAATATCCAAATCAACCATTTACAAAACACAAT 132
Db 26 -----TyrSerArgTyrProLeuAlaAsnLysProAsnGlnProLeuLysAsnThrAsn 43
QY 133 TACAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGTGATAATTTTCGAGACA 192

Db 44 TyrLysAspTrpLeuAsnValCysGlnAspAsnGlnGlnTyrGlyAsnAsnAlaGlyAsn 63
QY 193 TTTGCTAGTCTGATACAAATGCTGCAGTTAGTCAGGTACTATTGTATCCGGTACTCTG 252
Db 64 PheValSerSerGluThrIleValGlyValSerAlaGlyIleIleValValGlyThrMet 83
QY 253 TTAGCCGGTATAGTGGGCTCACTTCTATATCCGGACCGATAGGAATAAATAGGTGCTATA 312
Db 84 LeuGly-----AlaPheAlaAlaPro-----ValLeuAlaAlaGly 95
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Db 96 IleIleSerPheGlyThrLeuLeuProIlePheTrp---GlnGlySerAspProAlaAsn 114
QY 373 GTATGGACACAATTTATTAATAATGGGAGAAATTTTGTGTATACACCGTTTAACAGAA--- 429
Db 115 ValTrpGlnAspLeuLeuAsnIleGly-----GlyArgProIleGlnGluIle 130
QY 430 -----AGCATAAACAGCTAAAGTTACAAACTTTAGAGGATTTAGACAAATATTACAA 483
Db 131 AspLysAsnIleIleAsnValLeuThrSerIleValThrProIleLysAsnGlnLeuAsp 150
QY 484 AGCTATATAATACAGCATTTAGATGATTTGGAGAAATTTAAAGAGACTACAAAGCTCTCTG 543
Db 151 LysTyrGlnGluPhePheAspLysTrpGluProAlaArg----- 163
QY 544 CCACCATCATCAGCATTTACAAACAGCTGCTGCTCTTAAATATACGATTTTGAGAAATGTT 603
Db 164 -----ThrHisAlaAsnAlaLysAlaValHisAspLeuPheThrThrLeuGluProIle 181
QY 604 CACAAT-----GATTTTATTCGAGAAATACCTGGTTTCCAACTTGAACCTTATAAA 654
Db 182 IleAspLysAspLeuAspMetLeuLysAsnAlaSerTyrArgIleProThr----- 199
QY 655 ACGCTATTACTACTATTATGCGCAAGCTGCTAAATTTTCATTTTAAATTTTATTAACAACA 714
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QY 715 GTGTGTAATTTGGCTGATGAATGGAATGCAGATATACATCTTCCACAATTTGAACCTTAAT 774
Db 217 AlaAlaThrTyrTyrAsnIleTrp-----LeuGlnAsnGlnGlyIleAsnProSer 233
QY 775 GCTGGAACATCAGATGACTATTATAA---CTTTTAAAGAAATATATACCTTAATATAGT 831
Db 234 ThrPheAsnSerSerAsnTyrTyrGlnGlyTyrLeuLysArgLysIleGlnGluTyrThr 253
QY 832 AACTATTGTGCAAAATACCTATAGAGAGAGACTAAATAAACTTCGAAACGAACTTAATATG 891
Db 254 AspTyrCysIleGlnThrTyrAsnAlaGlyLeuThrMetIleArgThrAsnThrAsnAla 273
QY 892 AGATGGAGTATATTATGATGATTCGAGATATATGACTATTACTGTATTAGATACTATC 951
Db 274 ThrTrpAsnMetTyrAsnThrTyrArgLeuGluMetThrLeuThrValLeuAspLeuIle 293
QY 952 GCTCAATTTTCTTTTATGATATAAGAGATACAAAGATTCAATAGGAAGAAATAGGTGGC 1011
Db 294 AlaIlePheProAsnTyrAspProGluLysTyrProIle-----Gly 307
QY 1012 ATTAAAACTGAACCTTACAGAGAAATTTATACAACTCGAAATATAATTTTTCACCGCTTACT 1071
Db 308 ValLysSerGluLeuThrArgGluValTyr---ThrAsnValAsnSerAspThrPheArg 326
QY 1072 TACCTTGAATTTCAACCCCAATCTCGCTATATATGAAATATATTTAAACAGCTTCAGGCGTT 1131
Db 327 -----ThrIleThrGluLeuGluAsnGlyLeuThrArgAsnPro--- 339
QY 1132 AGATTATTTTTCATTTTATGATGAACCTTATATTTTATACAAAAAT----- 1176
Db 340 ThrLeuPheThrTrpIleAsnGlnGlyArgPheTyrThrArgAsnSerArgAspIleLeu 359
QY 1177 GAAACGCTAC-----GGGAATCGTTTGTGTTAGTTGCTATTTGCGAATCGTAAT 1218
Db 1177 GAAACGCTAC-----GGGAATCGTTTGTGTTAGTTGCTATTTGCGAATCGTAAT 1218

Db 281 IleValLeuPheProPheTyrAspValArgLeuTyrSerLys----- 294
QY 1009 GGCATTAAACTGAATTCACAGAGAAATTTATACAACTGAAATAAATTTTGACGCTTT 1068
Dy 295 GlyValIleThrGluLeuThrArgAspIlePheThrAspProIle---PheThrLeuAsn 313
QY 1069 ACTTACCTTGAAATTCACCCCAATCTCGCTATAATGGAATATAATTTAAACACGTTTCAGG 1128
Db 314 AlaLeuGlnGluTyrGlyProThrPheSerSerIleGluAsnSerIleArgLysPro--- 332
QY 1129 CTGAGTATATTTTCAATTTTAGACTTATATATTTATACAAA----- 1173
Db 333 ---HisLeuPheAspTyrLeuArgGlyIleGluPheHisThrArgLeuArgProGlyTyr 351
QY 1174 -----AATGAACGTACGGGAATCGTTTGTGTTGTTGTAATTCGGAATCGT 1215
Db 352 SerGlyLysAspSerPheAsnTyrTrpSerGlyAsnTyr-----ValGluThrArg 368
QY 1216 AATAGATCTACTTATGCTACGACGAGAACTGAAATATATATGGAAGAAGACAGGTCCA 1275
Db 369 ProSerIleGlySerAsnAspThrIleThrSerProPheTyrGlyAspLysSerIleGlu 388
QY 1276 CCCCAACAAAACTTTAATACCAATTTGAATCTCTATAAAGTTTCAATTTGTAACGTATAGA 1335
Db 389 ProlIleGlnLys-----LeuSerPheAspGlyGlnLysValTyr-----Arg 402
QY 1336 CAAGTA-----ACTCCTACTTCCCTTTCTCTAAC-----ATATACTTTACAAATTAAT 1383
Db 403 ThrIleAlaAsnThrAspIleAlaAlaPheProAspGlyLysIleTyrPheGlyValThr 422
QY 1384 CAAATTTGAATTTATTTAAATAATTCACCTAGTATATAATTA-----ACATATTCA 1434
Db 423 LysValAspPheSerGlnTyrAspAspGlnLysAsnGluThrSerThrGlnThrTyrAsp 442
QY 1435 GCT-----GGGGGGAAATTTATCTAATGATAAA-----AAA 1464
Db 443 SerLysArgTyrAsnGlyTyrLeuGlyAlaGlnAspSerIleAspGlnLeuProGlu 462
QY 1465 ACAACTGATTTTCAATTTCTGTAAAGAAAGACTGTAAACCAATATTAAATCCAAATGT 1524
Db 463 ThrThrAsp-----GluProLeuGluLys----- 470
QY 1525 TTACCAAGCTATATAGTTATAGTCATATTTATCCAGTTTCTTTATTTAATTTATCC 1584
Db 471 -----AlaTyrSerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGln 485
QY 1585 TATAAATTTGGATTAGCGCTAAATATATATATACAGGTGCATGAGTACGACACACAGT 1644
Db 486 AspArgArgGlyThrIle-----ProPhePheThr-----TyrThrHisArg 499
QY 1645 AGTGTTAATAGAAATATGCAATATCAGATAAATAATATACATGATCCAGCAATCAAA 1704
Db 500 SerValAspPhePheAsnThrIleAspAlaGluLysIleThrGlnLeuProValValLys 519
QY 1705 GGTAACAGCTTGTATACAACTCTAAGTGAATTTGAAGCACTGTGTACACAGGAGGAAC 1764
Db 520 AlaTyrAlaLeuSerSerGlyAlaSerIleIleGluGlyProGlyPheThrGlyLysAsn 539
QY 1765 TTGGTTTATTTACAA-----AGTCAAGGGCGTTTATAGAGATTACATGTAGAACT 1812
Db 540 LeuLeuPheLeuLysGluSerSerAsnSerIleAlaLysPheLysValThrLeuAsnSer 559
QY 1813 CCTAATCTCACAACTCTTATACATTTAGCTTGTGATACGCTACAAATGGTGTGGAAT 1872
Db 560 AlaAlaLeuLeuGlnArgTyrArgValArgIleArgTyrAlaSerThr----- 575
QY 1873 ACTCTCTCTATATATCTTTACATATACCAGGAGTAAATAGGAATACCACTCAACGATC 1932
Db 576 -----ThrAsnLeuArgLeuPheVal-----GlnAsnSer 585
QY 1933 AACCAACACTTTTCTGGTACAAATATATATATATTTACAATAC-----GGAGATTTTGGG 1986
Db 586 AsnAsnAspPheLeuValIleTyrIleAsnLysThrMetAsnIleAspGlyAspLeuThr 605

QY 1987 TAT-----TTCCAAATTTCCAGTACAGTACATTACTTTAATCGAATACCATTTT 2040
Db 606 TyrGlnThrPheAspPheAlaThrSer-----AsnSerAsnMetGlyPhe 620
QY 2041 ATATTTAATCGTCAGAT-----GTATCAAATTTCAATTTTA 2076
Db 621 SerGlyAspThrAsnAspPheIleIleGlyAlaGluSerPheValSerAsnGluLysIle 640
QY 2077 ATCATGATAAAATTTGAATTTATACCAAT 2106
Db 641 TyrIleAspLysIleGluPheIleProVal 650
RESULT 7
US-07-941-650A-4
; Sequence 4, Application US/07941650A
; Patent No. 6294184
; GENERAL INFORMATION:
; APPLICANT: Uveda, Kendrick A.
; APPLICANT: Bradfisch, Gregory A.
; TITLE OF INVENTION: Process for Controlling Lepidopteran Pests
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/941,650A
; FILING DATE: 19920908
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/758,020
; FILING DATE: 12-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/658,935
; FILING DATE: 21-FEB-1991
; APPLICATION NUMBER: US 07/642,112
; FILING DATE: 16-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 651 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: tolworthi
; INDIVIDUAL ISOLATE: 43f
; IMMEDIATE SOURCE:
; CLONE: E. coli XL1-Blue (pML98-4), NRRL B-18291
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..651
US-07-941-650A-4

Alignment Scores:

Pred. No.: 1.37e-55 Length: 651
Score: 706.00 Matches: 216
Percent Similarity: 44.27% Conservative: 116
Best Local Similarity: 28.80% Mismatches: 270
Query Match: 17.92% Indels: 148
DB: 2 Gaps: 31

US-10-782-570-1 (1-2235) x US-07-941-650A-4 (1-651)

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QY 1 GTGAATCAAAATATAATAATGAATATGAGATTATCGAT-----TCAAAGAAATTATCTTAT 57
DB 1 MetAenProAasnArgSerGluTyrAspThrIleLysValThrProAasnSerGluLeu 20
QY 58 CTTCTTAACAGAAATATTGATCATTTCTAGATACCTTTACACAAATAATCCAAATCAACA 117
DB 21 ProThrAen-----HisAenGlnTyrProLeuAlaAaspAasnProAasnSerThr 36
QY 118 TTACAAAACACAAATTTACAAAGAGTGGCTCAATATGTGTCAAGGGAATACACAAATATG 177
DB 37 LeuGluGluLeuAasnTyrLysGluPheLeuArgMetThrAlaAaspAasnSerThr----- 54
QY 178 GATAATTTCCGACAAATTTGCTAGTCTGCTGATACAAATTTGCTGCGAGTTAGTGCAGTACTATT 237
DB 55 -----GluValLeuAaspSerSerThrValLysAaspAlaValGlyThrGlyIleSer 71
QY 238 GTATCCGCTACTCTGTAGCCGGTATAGTGGCTCACTTCTATATCCGACCGCATAGGA 297
DB 72 ValValGlyGlnIleLeuGlyValValGly-----ValPro 83
QY 298 ATAATAGTGTCTATAATAATCTTTTGGTACCCCTAATCACTGTCTTTTGGCCCGCGGA 357
DB 84 PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAenAlaIleTyrProSer--- 102
QY 358 GAACAAGACAAACAGTAGTAGACACAAATTTATAAATGGGAGAAATTTTGTTCATACA 417
DB 103 -----AaspAaspProTyrLysAlaPheMetalGlnValGluValLeuIleAaspLys 120
QY 418 CGTTTAAACAGAAAGCATAAACAGCTAAAGTTACAACTTTAGAGAGGATTTAGACAAATA 477
DB 121 LysIleGluGluTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAasnAen 140
QY 478 TTACAAAGCTATAATACAGCATTAGATGATTCGAGAAATTTAAAGAGCTACAAAGCTCT 537
DB 141 PheGluAaspTyrValAasnAlaLeuAaspSerTyrLysLys----- 153
QY 538 GGATTTACCAATCATCAGCATTAACAACAGCTGCTTGACTCTTTAAATACAGATTGAG 597
DB 154 ---AlaProValAasnLeuArgSerArgSerGlnAaspArgIleArgGluLeuPheSer 172
QY 598 ATGTTCACAAATGATTTTATTCGAGNAATACCTGGTTTCCAACTTGAACCTTATAAAGC 657
DB 173 GlnAlaGluSerHisPheArgAasnSerMetProSerPheAlaValSerLysPheGluVal 192
QY 658 CTATTACTACTATTATTCGCAAGCTGCTTAATTTTCAATTTAAATTTTATTAACAACAGGT 717
DB 193 LeuPheLeuProThrTyrAlaGlnAlaAasnThrHisLeuLeuLeuLeuLysaspAla 212
QY 718 GCTGAATTCGGCTGATGAATGGAATGCAGATATACATCTTCTCAAAATGCACTAATGCT 777
DB 213 GlnValPheGlyGluGluTyrGlyTyr----- 221
QY 778 GGAACATCAGATGAC-----TATTATAACTTTTAAAGAAAATATACCTAAATAT 828
DB 222 ---SerSerGluAaspIleAlaGluPheTyrGlnArgGlnLeuLysLeuThrGlnGlnTyr 240
QY 829 AGTAACATTATTTGGCAATACCTATACAGAGGACTAAATAAATCTCGAAACCAACCTAAT 888
DB 241 ThrAaspHisCysValAasnTyrPyrAasnValGlyLeuAasnSerLeuArgGlySerThrTyr 260
QY 889 ATGAGATGGAGTATATTATTAATGATTATCGAAGATATATGACTATTATCTATTAGTACT 948
DB 261 AspAlaTyrValLysPheAasnArgPheArgArgGluMetThrLeuThrValLeuAaspLeu 280
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QY 949 ATCCGCTCAATTTCTTTTATGATATAAAGAGATACAAAGATTCAATAGGAAGATAGGT 1008
DB 281 IleValLeuPheProPheTyrAspValArgLeuTyrSerLys----- 294
QY 1009 GGCATTAATAAATCAACTTACAAAGAAATTTATCAACTGAATTAATTTTACCGCTCTT 1068
DB 295 GlyValLysThrGluLeuThrArgAaspIlePheThrAaspProIle---PheThrLeuAen 313
QY 1069 ACTTACCTTGAATTTCAACCCCAATCTCGCTATAATGGAATATAATTTAACAGTTTCAGG 1128
DB 314 AlaLeuGlnGluTyrGlyProThrPheSerSerIleGluAasnSerIleArgLysPro--- 332
QY 1129 CTTAGATTATTTTCAATTTTAGATGAACCTTATATTTATACAAA----- 1173
DB 333 ---HisLeuPheAaspTyrLeuArgGlyIleGluPheHisThrArgLeuArgProGlyTyr 351
QY 1174 -----AATGAACGTACCGGAATCGTTTGTAGTTGGTATTTCGGAATCGT 1215
DB 352 SerGlyLysAaspSerPheAasnTyrTyrSerGlyAasnTyr-----ValGluThrArg 368
QY 1216 AATAGATCTACTATGCTACGACAGAACTGAAATATATATATGGAAGAAGACAGGTCCA 1275
DB 369 ProSerIleGlySerAasnAaspThrIleThrSerProPheTyrGlyAaspLysSerIleGlu 388
QY 1276 CCCCAACACAAAACCTTTTAATACCAATTCATTAAGTTTCAATTTGTAACGTGATGA 1335
DB 389 ProlIleGlnLys-----LeuSerPheAaspGlyGlnLysValTyr-----Arg 402
QY 1336 CAAGTA-----ACTCTACTTCCCTTTCTCTAAC-----ATATACTTTACAATTAAT 1383
DB 403 ThrIleAasnThrAaspIleAlaPheProAaspGlyLysIleTyrPheGlyValThr 422
QY 1384 CAATTTGAACCTTTATTTAAATAATTTACCTAGTAATAAATTA-----ACATATTCA 1434
DB 423 LysValAaspPheSerGlnTyrAaspAaspGlnLysAasnGluThrSerThrGlnThrTyrAap 442
QY 1435 GCT-----GGGGGGAATTTTCTAATGATAAA-----AAA 1464
DB 443 SerLysArgTyrAasnGlyTyrLeuGlyAlaGlnAaspSerIleAaspGlnLeuProGlu 462
QY 1465 ACAACTGATTTTCAATTTCTGTGTAATAAAGAGCTGTAAACCAATTTAATCAAAATGCT 1524
DB 463 ThrThrAasp-----GluProLeuGluLys----- 470
QY 1525 TTACCAAGCTATATAGTTATAGTATATATTTATCCAGTTTCTTTTATTTAATTTATTC 1584
DB 471 -----AlaTyrSerHisGlnLeuAasnTyrAlaGluCysPheLeuMetGln 485
QY 1585 TATAAAATTTGGATTAGCGCTAAATATATATATACAGGTGCGATTAGGATGACACACAGT 1644
DB 486 AspArgArgGlyThrIle-----ProPhePheThr-----TyrThrHisArg 499
QY 1645 AGTGTAAATAGAAATAATGCAATATCAGATAAATAATTAATATCAATGATCCAGCAATCAAA 1704
DB 500 SerValAaspPheAasnThrIleAaspAlaGluLysIleThrGlnLeuProValLys 519
QY 1705 GGTAACAGCTCTTGATACAACTCTAAGGTAAATGAAGGACCTGCTCATACAGAGGAAAC 1764
DB 520 AlaTyrAlaLeuSerSerGlyAlaSerIleIleGluGlyProGlyPheThrGlyGlyAen 539
QY 1765 TTGGTTTATTTTACAA-----AGTCAAGGGCGTTTATAGAGATATACATGTAAGT 1812
DB 540 LeuLeuPheLeuLysGluSerSerAasnSerIleAlaLysPheLysValThrLeuAasnSer 559
QY 1813 CCTAATTTCTACAAATCTTATTTACATTTAGACTTTCGATTCAGTACAAATGGTGTGGAAT 1872
DB 560 AlaAlaLeuLeuGlnArgTyrArgValArgIleAsgTyrAlaSerThr----- 575
QY 1873 ACTCTTCTTAATATATCTCTTACATATACAGAGGATTAATAGGAATACCACTCAACGCTC 1932
DB 576 -----ThrAasnLeuArgLeuPheVal-----GlnAasnSer 585
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Db 629 SerGlyAspThrAsnAspPheIleIleGlyAlaGluSerPheValSerAsnGluLysIle 646

Qy 2077 ATCATTCATATAAAATTGGAATTTATACCAATT 2106
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Db 649 TyrIleAspLysIleGluPheIleProVal 658

RESULT 9
US-08-993-722A-112
Sequence 112, Application US/08993722A
Patent No. 6060594
GENERAL INFORMATION:
APPLICANT: English, Leigh H.
APPLICANT: Brussock, Susan M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Bryson, James W.
APPLICANT: Kuleza, Caroline A.
APPLICANT: Kuleza, Frederick S.
APPLICANT: Slatin, Stephen L.
APPLICANT: Von Tersch, Michael A.
APPLICANT: Romano, Charles
TITLE OF INVENTION: NUCLEIC ACID SEGMENTS ENCODING MODIFIED
TITLE OF INVENTION: COLEOPTERAN-TOXIC CRYSTAL PROTEINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/993,722A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO149
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3106
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 659 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-993-722A-112

Alignment Scores:
Pred. No.: 1.38e-55 Length: 659
Score: 706.00 Matches: 216
Percent Similarity: 44.27% Conservative: 116
Best Local Similarity: 28.80% Mismatches: 270
Query Match: 17.92% Indels: 148
DB: 2 Gaps: 31

US-10-782-570-1 (1-2235) x US-08-993-722A-112 (1-659)

Qy 1 GTGAATCAAAATATAATGAATATGAGATTATCGAT---TCAAGAAATTTATCTTAT 57
:||||| :||||| :||||| :||||| :|||
Db 9 MetaAsnProAsnAsnArgSerGluTyrAspThrIleLysValThrProAsnSerGluLeu 28
58 CCTTCTACAGAAATATTGATCATTTAGATACCTTACACAAATACCCCTTACACAAATATCAATCAACCA 117
:||||| :||||| :||||| :||||| :|||
Db 29 ProThrAsn-----HisAsnGlnTyrProLeuAlaAspAsnProAsnSerThr 44
118 TTACAAAACACAAATTAACAAGAGTGGCTCAATATGTGTCAAGGGGAATACACATATGTT 177

[illegible]

Db	360	SerGlyLyAspSerPheAsnTyrTrpSerGlyAsnTyr-----ValGluThrArg	376
Qy	1216	AATAGATCTATTATGCTACGACGAGGAACGTAAATTATATATATGAGAAAGAACAGGTCCA	1275
Db	377	ProSerIleGlySerAsnAspThrIleThrSerProPheTyrGlyAspLysSerIleGlu	396
Qy	1276	CCCAACAACAAAACCTTTTAATACCAATTCCTATAAAAGTTTCAATTGCTAACTGATGA	1335
Db	397	ProIleGlnLys-----LeuSerPheAspGlyGlnLysValTyr-----Arg	410
Qy	1336	CAAGTA-----ACTCCTACTTCCCTTTTCCCTAAC-----ATATACTTTTCAATTAAT	1383
Db	411	ThrIleAlaAsnThrAspIleAlaAlaPheProAspGlyLysIleTyrPheGlyValThr	430
Qy	1384	CAAAATCGAACTTTATTTAAATAATTCACCTAGTAATAAAATTA-----ACATATTCA	1434
Db	431	LysValAspPheSerGlnTyrAspAspGlnLysAsnGluThrSerThrGlnThrTyrAsp	450
Qy	1435	GCT-----GGGGGAATTTATCTAATCATAA-----AAA	1464
Db	451	SerLysArgTyrAsnGlyTyrLeuGlyAlaGlnAspSerIleAspGlnLeuProGlu	470
Qy	1465	ACAACTCATTTTCAATTTCTCTGTAATAAAAGACTGTAAACCAATTATTATCCAAATGT	1524
Db	471	ThrThrAsp-----GluProLeuGluLys-----	478
Qy	1525	TTACCAAGCTATAATAGTATAGTATCATATTTTATCCAGTTTCTTTATTATTATTC	1584
Db	479	-----AlaTyrSerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGln	493
Qy	1585	TATAAAATTCGATTACGGCTAAATATATTATATACAGGTGCATTAGGATGGACACACAGT	1644
Db	494	AspArgGlyThrIle-----ProPhePheThr-----TrpThrHisArg	507
Qy	1645	AGTGTTAATAGAATAATGCAATATCAGATAAAATAATACAAATGATCCAGCAATCAA	1704
Db	508	SerValAspPhePheAsnThrIleAspAlaGluLysIleThrGlnLeuProValValLys	527
Qy	1705	GGTAACAGCTCTTGATACAACTCTAAGTAAATTGAAGGACCTGGTGCATACAGAGGAAC	1764
Db	528	AlaTyrAlaLeuSerSerGlyAlaSerIleIleGluGlyProGlyPheThrGlyGlyAsn	547
Qy	1765	TTGGTTTATTATTCACAA-----AGTCAAGGGCGTTTAGAGATTACATGTAGAACT	1812
Db	548	LeuLeuPheLeuLysGluSerSerAsnSerIleAlaLysPheLysValThrLeuAsnSer	567
Qy	1813	CCTAATTTCTACAACTCTTATTACACTTCGATACGCTACAAATGGTCTCGGAAT	1872
Db	568	AlaAlaLeuLeuGlnArgTyrArgValAlaGileArgTyrAlaSerThr-----	583
Qy	1873	ACTCTTCCTAATATATCTCTTACAAATACCAGGAGTAATAGGAATACCACCTCAACGACTC	1932
Db	584	-----ThrAsnLeuArgLeuPheVal-----GlnAsnSer	593
Qy	1933	AACAACACTTTTTCTCGTACAAATATATAATATTTACAATAC-----GGAGATTTGGG	1986
Db	594	AsnAsnAspPheLeuValIleTyrIleAsnLysThrMetAsnIleAspGlyAspLeuThr	613
Qy	1987	TAT-----TTCAAATTTCCAGTACAGTAACTTACCTTTTAATCGAAACATACATTT	2040
Db	614	TyrGlnThrPheAspPheAlaThrSer-----AsnSerAsnMetGlyPhe	628
Qy	2041	ATATTTAATCGTGCAGAT-----GTATCAATTCAAATTTTA	2076
Db	629	SerGlyAspThrAsnAspPheIleIleGlyAlaGluSerPheValSerAsnGluLysIle	648
Qy	2077	ATCATTGATAAAATGAATTTATACCAATT	2106
Db	649	TyrIleAspLysIleGluPheIleProVal	658

RESULT 10
US-08-993-170A-112
; Sequence 112, Application US/08993170A

Db 129 LysLeuGluGluTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAsnAen 148
Qy 478 TTACAAGCTATAATACAGCATAGATGCGAGAAATTAATAAGACTACAGCTCCT 537
Db 149 PheGluAspTyrValAsnAlaLeuAspSerTrpLysLys----- 161
Qy 538 GGATTACCACCATCATCAGCATACACAGCTGCTTGAATCTTAAATACGATTTCGAG 597
Db 162 ---AlaProValAsnLeuArgSerArgArgSerGlnAspArgGileArgGluLeuPheSer 180
Qy 598 AATGTTCAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAACCTTATAAAGC 657
Db 181 GlnAlaGluSerHisPheArgAsnSerMetProSerPheAlaValSerLysPheGluVal 200
Qy 658 CTATTACTACCTATTATTCGCGAAGCTGCTAAATTTTCAATTTTAAATTTATTAACAAGGT 717
Db 201 LeuPheLeuProThrTyrAlaGlnAlaAlaAsnThrHisLeuLeuLeuLysAspAla 220
Qy 718 GCTGAATTGGCTGATGAATGGAATGCAGATATACATCTCTCACAATTTGAACTTAATGCT 777
Db 221 GlnValPheGlyGluGluTrpGlyTyr----- 229
Qy 778 GGAACATCAGATGAC-----TATTATAAATCTTTTAAAGAAATATATACCTAAATAT 828
Db 230 ---SerSerGluAspIleAlaGluPheTyrGlnArgGlnLeuLysLeuThrGlnGlnTyr 248
Qy 829 ACTAATCTATTTGCGAAATACCTATAGAGAAGACTAAATAAATCTTGAACGAACTTAAT 888
Db 249 ThrAspHisCysValAsnTrpTyrAsnValGlyLeuAsnSerLeuArgLysSerThrTyr 268
Qy 889 ATGAGATCGAGTATATTAATGATTCGAGATATATGATCTATTCATCTGATTTAGATACT 948
Db 289 AspAlaTrpValLysPheAsnArgPheArgArgGluMetThrLeuThrValLeuAspLeu 288
Qy 949 ATCGCTCAATTTCTTTTATGATATAAGAGATACAAAGATTCATAGGAAGATAGGT 1008
Db 289 IleValLeuPheProPheTyrAspValArgLeuTyrSerLys----- 302
Qy 1009 GGCATTAATCACTTACAGAGAAATTTATACACTGAAATTAATTTGACGCTTT 1068
Db 303 GlyValLysThrGluLeuThrArgAspIlePheThrAspProIle---PheThrLeuAsn 321
Qy 1069 ACTTACCTTGAATTCACCCCAATCTCGTATATAGGAATATATTTAACAGCTTCAGGG 1128
Db 322 AlaLeuGlnGluTyrGlyProThrPheSerSerIleGluAsnSerIleArgLysPro--- 340
Qy 1129 CTGATGATTTTTCATTTTATAGATCAACTTATATTTTATACAAA----- 1173
Db 341 ---HisLeuPheAspTyrLeuArgGlyIleGluPheHisThrArgLeuArgProGlyTyr 359
Qy 1174 -----AATGAACGTCAGGGAATCGTTAGTTGGTATTCGGAATCGT 1215
Db 360 SerGlyLysAspSerPheAsnTyrTrpSerGlyAsnTyr-----ValGluThrArg 376
Qy 1216 AATAGATCTACTTATGCTACGACGAAGTGAATATATATATGGAAGAACAGCTCCA 1275
Db 377 ProSerIleGlySerAsnAspThrIleThrSerProPheTyrGlyAspLysSerIleGlu 396
Qy 1276 CCCACACAAACAACTTAAATCACTTCAATCCTATAAAGTTTCAATGTAACCTGATAGA 1335
Db 397 ProIleGlnLys-----LeuSerPheAspGlyGlnLysValTyr-----Arg 410
Qy 1336 CAAGTA-----ACTGCTACTTCCCTTTTCTTAAC-----ATATCTTTCAATTAAT 1383
Db 411 ThrIleAlaAsnThrAspIleAlaAlaPheProAspGlyLysIleTyrPheGlyValThr 430
Qy 1384 CAATTTGAATTTTATTAATAATTTCACTAGTAAATTA-----ACATATCA 1434
Db 431 LysValAspPheSerGlnTyrAspAspGlnLysAsnGluThrSerThrGlnThrTyrAsp 450
Qy 1435 GCT-----GGGGGAATTTTATCTTAATGATAAA-----AAA 1464
Db 1435 GCT-----

Db 451 SerLysArgTyrAsnGlyTyrLeuGlyAlaGlnAspSerIleAspGlnLeuProProGlu 470
Qy 1465 ACRACTGATTTTCAATTTCTGTAATAAAGAGACTGTAAACCAATTTATTAATCCAAATGT 1524
Db 471 ThrThrAsp-----GluProLeuGluLys----- 478
Qy 1525 TTACCAAGCTATATAGATAGTATAGTATATTTATCCAGCTTTTCTTTTATTAATTTATTC 1584
Db 479 -----AlaTyrSerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGln 493
Qy 1585 TATAAATGATAGTAGCGCTAAATATATATATATACAGGTGATAGGATGACACACAGT 1644
Db 494 AspArgArgGlyThrIle-----ProPhePheThr-----TipThrHisArg 507
Qy 1645 AGTCTTAAAGAAATATGCAATATCAGATAAATAATTAACAATGATCCAGCAATCAAA 1704
Db 508 SerValAspPhePheAsnThrIleAspAlaGluLysIleThrGlnLeuProValLys 527
Qy 1705 GGTAACAGCTCTTGATACAAACTCTAAGCTAATTCAGAGCCTGCTCATACAGGAGGAAC 1764
Db 528 AlaTyrAlaLeuSerSerGlyAlaSerIleIleGluGlyProGlyPheThrGlyGlyAsn 547
Qy 1765 TTGCTTTATTTACAA-----AGTCAAGGGCGTTTAGAGATTACATAGTAGAAT 1812
Db 548 LeuLeuPheLeuLysGluSerSerAsnSerIleAlaLysPheLysValThrLeuAsnSer 567
Qy 1813 CCTAATTTCTACAACTCTTATACATTTAGCTTCGATACGCTACAAATGCTGCTGGAAT 1872
Db 568 AlaAlaLeuLeuGlnArgTyrArgValArgIleArgTyrAlaSerThr----- 583
Qy 1873 ACTCTCTTAATATATCTCTTCAATACCAAGAGTAAAGGAATACCACTCAACGACTC 1932
Db 584 -----ThrAsnLeuArgLeuPheVal-----GlnAsnSer 593
Qy 1933 AACCAACTTTTCTGTCACAAATTTATAATTAATTTACAATAC-----GGAGATTTTGG 1986
Db 594 AsnAsnAspPheLeuValIleTyrIleAsnLysThrMetAsnIleAspGlyAspLeuThr 613
Qy 1987 TAT-----TTCCAATTTCCAAGTACAGATACATTCCTTTAATCGAAACATACCATTT 2040
Db 614 TyrGlnThrPheAspPheAlaThrSer-----AsnSerAsnMetGlyPhe 628
Qy 2041 ATATTTAATCTGTCAGAT-----GTATCAAAATTTCAATTTTA 2076
Db 629 SerGlyAspThrAsnAspPheIleIleGlyAlaGluSerPheValSerAsnGluLysIle 648
Qy 2077 ATCATGATAAAATTTGAATTTTATACCAAT 2106
Db 649 TyrIleAspLysIleGluPheIleProVal 658
RESULT 12
US-09-427-770-112
; Sequence 112, Application US/09427770
; Patent No. 6620988
; GENERAL INFORMATION:
; APPLICANT: English, Leigh H.
; APPLICANT: Bruseock, Susan M.
; APPLICANT: Malvar, Thomas W.
; APPLICANT: Bryson, James W.
; APPLICANT: Kulesza, Caroline A.
; APPLICANT: Walters, Frederick S.
; APPLICANT: Slatin, Stephen L.
; APPLICANT: Von Teresh, Michael A.
; APPLICANT: Romano, Charles
; TITLE OF INVENTION: NUCLEIC ACID SEGMENTS ENCODING MODIFIED
; TITLE OF INVENTION: COLEOPTERAN-TOXIC CRYSTAL PROTEINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA

1525 TTACCAAGCTATAAGTATTAGTATCATATTTATCCAGTTTCTTTTATTATTAATTTATCC 1584
479AlatySerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGln 493
1585 TATAAAATGGATTAGCCGCTAAATATATATATACAGGTGCTAGGATGACACACAGT 1644
494 AspArgGlyThrIle-----ProPhePheThr-----TyrThrHisArg 507
1645 AGTGTATATAGATAAATAGCATATCATAGATAAATAATATACATGATCCAGCATCAAA 1704
508 SerValAspPhePheAsnThrIleAspAlaGluTyrIleThrGlnLeuProValVallys 527
1705 GGTACAGCTCTGATACAACTCTAAGGTAAATGAAGCAGCTGGTCATACAGGAGGAAC 1764
528 AlatyAlaLeuSerSerGlyAlaSerIleIleGluGlyProGlyPheThrGlyGlyAsn 547
1765 TTGGTTTATTTACAA-----AGTCAAGGCGCTTTAGAGATTACATGATAGAACT 1812
548 LeuLeuPheLeuLysGluSerSerAsnSerIleAlaLysPheLysValThrLeuAsnSer 567
1813 CCTAATCTCACATCTTATACATTAGACTTCGATACGCTACAAATGGTGTGCTGAAT 1872
568 AlaAlaLeuLeuGlnArgTyrArgValArgIleArgTyrAlaSerThr----- 583
1873 ACTCTTCCTAATATATCTCTTACAATACAGGAGTAATAGGAATACCACTCAACGACTC 1932
584 -----ThrAsnLeuArgLeuPheVal-----GlnAsnSer 593
1933 AACAACTCTTTCTGGTACAAATATATATATTTTACAATAC-----GGAGATTTTGGG 1986
594 AsnAsnAspPheLeuValIleTyrIleAsnLysThrMetAsnIleAspGlyAspLeuThr 613
1987 TAT-----TTCCAATTTCCAAGTACAGTAACATTTACCTTTAAATCGAAACATACATTT 2040
614 TyrGlnThrPheAspPheAlaThrSer-----AsnSerAsnMetGlyPhe 628
2041 ATATTTAATCGGCAGAT-----GTATCAATTTCAATTTTA 2076
629 SerGlyAspThrAsnAspPheIleIleGlyAlaGluSerPheValSerAsnGluLysIle 648
2077 ATCATTTGATAAATTTGAATTTTATACCAATT 2106
649 TyrIleAspLysIleGluPheIleProVal 658

RESULT 13

US-09-427-769-112
Sequence 112, Application US/09427769
Patent No. 6642030

GENERAL INFORMATION:

APPLICANT: English, Leigh H.
APPLICANT: Brussock, Susan M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Bryson, James W.
APPLICANT: Kulesza, Caroline A.
APPLICANT: Walters, Frederick S.
APPLICANT: Statin, Stephen L.
APPLICANT: Von Tersch, Michael A.
APPLICANT: Romano, Charles

TITLE OF INVENTION: NUCLEIC ACID SEGMENTS ENCODING MODIFIED
COLLOIDAL-TOXIC CRYSTAL PROTEINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/427,769
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,722
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:149
TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3106
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 112:

SEQUENCE CHARACTERISTICS:
LENGTH: 659 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

US-09-427-769-112

Alignment Scores:
Pred. No.: 1.38e-55 Length: 659
Score: 706.00 Matches: 216
Percent Similarity: 44.27% Conservative: 116
Best Local Similarity: 28.80% Mismatches: 270
Query Match: 17.92% Indels: 148
DB: 2 Gaps: 31

US-10-782-570-1 (1-2235) x US-09-427-769-112 (1-659)

QY 1 GTGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 57
DB 9 MetAsnProAsnAsnArgSerGluTyrAspThrIleLysValThrProAsnSerGluLeu 28
QY 58 CCTTCTTAACAGAAATATTGATCATCTTAGATACCTTTACACAAATAATCAAAATCAACA 117
DB 29 ProThrAsn-----HisAsnGlnTyrProLeuAlaAspAsnProAsnSerThr 44
QY 118 TTACAAACACAAATTAACAAAGTGGCTCAATATGTGTCAAGGGAATACACAAATATGGT 177
DB 45 LeuGluGluLeuAsnTyrLysGluPheLeuArgMetThrAlaAspAsnSerThr----- 62
QY 178 GATTAATTCGACACATTTGCTAGTCTGATACATAATGTCTGCAGTTAGTCAGGTACTATT 237
DB 63 -----GluValLeuAspSerSerThrValLysAspAlaValGlyThrGlyLysSer 79
QY 238 GTATCCGGTACTCTGTAGCCGGTATAGTGGGCTCACTTCTATATCCGACCGATAGGA 297
DB 80 ValValGlyGlnIleLeuGlyValValGly-----ValPro 91
QY 298 ATAATAGGTGCTATAATTAATATCTTTTGGTACCCTTAATCATCTGTCTTTGGCCCGGGA 357
DB 92 PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnAlaIleTyrProSer--- 110
QY 358 GAACAGACAAACAGTATGACACAAATTTATAAATGGGGAATTTTGTTCATACA 417
DB 111 -----AspAlaAspProTyrPheAlaPheMetAlaGlnValGluValLeuIleAspLys 128
QY 418 CGTTTACAGAAAGCATAAACAGCTAAAGTTTACAAACTTTAGAGAGGATTTAGACAAATA 477
DB 129 LysIleGluGluTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAsnAsn 148
QY 478 TTACAAAGCTATAATACAGCATTAATGATGGAGAAAATTTAAAGAGCTACACAGCTCT 537
DB 149 PheGluAspTyrValAsnAlaLeuAspSerTyrLysLys----- 161
QY 538 GGATTTACCAACCATCATCAGCATTAACACAGCTGCTTGTACTCTTAAATACGATTGAG 597
DB 162 ---AlaProValAsnLeuArgSerArgSerGlnAspArgIleArgGluLeuPheSer 180
QY 598 AATGTTCAATGATTTTATTTCGAGAAATACCTGCTGTTCCAACTTGGAACTTATAAAACG 657

REFERENCE/DOCKET NUMBER: MRCO:151

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 110:

SEQUENCE CHARACTERISTICS:

LENGTH: 652 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-996-441B-110

Alignment Scores:

Pred. No.:	4,82e-55	Length:	652
Score:	700.00	Matches:	216
Percent Similarity:	44.58%	Conservative:	117
Best Local Similarity:	28.92%	Mismatches:	272
Query Match:	17.77%	Indels:	142
DB:	2	Gaps:	32

US-10-782-570-1 (1-2235) x US-08-996-441B-110 (1-652)

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QY 1 GTGAATCAAAATAATAAATAAGATATGAGATATCGAT-----TCAAAGAAATTTATCTTAT 57
Db 1 MetAsnProAsnAsnArgSerGluHisAspThrIleLysValThrProAsnSerGluLeu 20
QY 58 CCTTCTACAGAAATTTGATCATCTAGATACCTTACACAAATTAATCCAAATCAACCA 117
Db 21 ProThrAsn-----HisAsnGlnTyrProLeuAlaAspAsnProAsnSerThr 36
QY 118 TTCAAAACACAAATTAACAAAGAGTGGCTCAATATGTCTCAA--GGGAATACACAATAT 174
Db 37 LeuGluGluLeuAsnTyrLysGluPheLeuArgMetThrGluAspSerSerThrGluVal 56
QY 175 GGTGATAATTCGAGACATTTGCTAGTCTGATACAAATGTCT---GCAGTAGTCAGGT 231
Db 57 LeuAspAsn-----SerThrValLysAspAlaValGlyThrGly 69
QY 232 ACTATTGTATCCGTACTCTGTAGCCGGTATAGTGGGCTCACTTCTATATCCGACCG 291
Db 70 IleSerValValGlyGlnIleLeuGlyValValGly----- 81
QY 292 ATAGAATAATAGGTGCTATATAATATCTTTGGTACCCTAATCACTGTCTTTGGGCC 351
Db 82 ValProPheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAspThrIleTyrPro 101
QY 352 GCGGAGAACAGACAAACAGTAGTAGACACAATTTATTAATAAGGGAGAAATTTTGT 411
Db 102 Ser-----AspAlaAspProTyrLysAlaPheMetAlaGlnValGluValLeuIle 118
QY 412 GATACACCGTTACAGAAAGCATAAAGCAGCTAAAGTTACAACTTTAGAGAGTTAGA 471
Db 119 AspLysLysIleGluGlyTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGln 138
QY 472 CAAATATTACAAAGCTATAATAACAGCATTAGATGATTCGAGAAATATAAAGAGCTACAA 531
Db 139 AsnAsnPheGluAspTyrValAsnAlaLeuAsnSerTyrLysLys----- 153
QY 532 GCTCCTGGATTACCAATCATCATGACATTTACAAAGCTGCTTGACTCTTTAAATACGA 591
Db 154 -----ThrProLeuSerLeuArgSerLysArgSerGlnAspArgIleArgGluLeu 170
QY 592 TTTGAGATGTTCAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAACCTTAT 651
Db 171 PheSerGlnAlaGluSerHisPheArgAsnSerMetProSerPheAlaValSerLysPhe 190
QY 652 AAAACGCTATTACTACTATTATTCGCAAGCTGCTAAATTTTCATTTAAATTTATTACAA 711
Db 191 GluValLeuPheLeuProThrTyrAlaGlnAlaAlaAsnThrHisLeuLeuLeuLys 210
QY 712 CAAGGTGCTGAATTCGGCTGATGAATGGAAATGCAGATATACATCCTTTCACAAATTCGACCT 771
Db 211 AspAlaGlnValPheGlyGluGlyTyrGlySer----- 222

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QY 772 AATGCTGGAACATCAGATGACTATTATAAACTTTTAAAGAAAATATATACCTAAATATAGT 831
Db 223 SerGluAspValAlaGluPheTyrHisArgGlnLeuLysLeuThr---GlnGlnTyrThr 241
QY 832 AACTATTGTGCAATACCTATAGAGAAGAGCTAAATAAACTTCGAAGAACCTAAATATG 891
Db 242 AspHisCysValAsnTyrAsnValGlyLeuAsnGlyLeuArgGlySerThrTyrAsp 261
QY 892 AGATGGAGTATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGATCATC 951
Db 262 AlaTyrValLysPheAsnArgPheArgGluMetThrLeuThrValLeuAspLeuIle 281
QY 952 GCTCAATTTCTTTTATGATATAAGAGATACAAAGATTCAATAGGAAGAAATAGGTGGC 1011
Db 282 ValLeuPheProPheTyrAspValArgLeuTyrSerLys-----Gly 295
QY 1012 ATTAAACTGAACCTTACAGAGAAATTTATACAACTGAATATAAATTTTGACCGCTTACT 1071
Db 296 ValLysThrGluLeuThrArgAspIlePheThrAspProIle---PheSerLeuAsnThr 314
QY 1072 TACCTTGAATTCACCAATCTCGCTATATATGAATATATTTAAACACGTTAGGGCTT 1131
Db 315 LeuGlnGluTyrGlyProThrPheLeuSerIleGluAsnSerIleArgLysPro----- 332
QY 1132 AGATTATTTTCATTTTAGATGAACCTTATATTTTATACAAA----- 1173
Db 333 HisLeuPheAspTyrLeuGlnGlyIleGluPheHisThrArgLeuGlnProGlyTyrSer 352
QY 1174 -----AATGAACGTCACGGGAATCGTTAGTTAGTTATTCGAAATCGTAAT 1218
Db 353 GlyLysAspSerPheAsnTyrTyrSerGlyAsnTyr-----ValGluThrArgPro 369
QY 1219 AGATCTACTATGCTACGACAGGAACCTGAAATATATATATATGAGAAAGAACAGGTCCACC 1278
Db 370 SerIleGlySerSerLysThrIleThrSerProPheTyrGlyAspLysSerThrGluPro 389
QY 1279 ACAACAAAACCTTAAATACCACTTCAATCCTATATAAGATTTCAATGTAACTGATAGACAA 1338
Db 390 ValGlnLys-----LeuSerPheAspGlyGlnLysValTyr-----ArgThr 403
QY 1339 GTA-----ACTCCTACTTCCCTTTTCTTAAC-----ATATACTTTTCAATTAATCAA 1386
Db 404 IleAlaAsnThrAspValAlaAlaTyrProAsnGlyLysIleTyrPheGlyValThrLys 423
QY 1387 ATTGAACCTTATTAATAATTCACCTAGTATTAATAATTA-----ACATATTCAGCT 1437
Db 424 ValAspPheSerGlnTyrAspAspGlnLysAsnGluThrSerThrGlnThrTyrAspSer 443
QY 1438 -----GGGGGAATTTATCTAATGATAAA-----AAAAACA 1467
Db 444 LysArgAsnAsnGlyHisValGlyAlaGlnAspSerIleAspGlnLeuProGluThr 463
QY 1468 ACTGATTTTCAATTTCTGTAAATAAAGACGTGTAACCAATTTATTAATCCAAATTTGTTA 1527
Db 464 ThrAsp-----GluProLeuGluLys----- 470
QY 1528 CCAAGCTATATAGTTATGATCATATTTATCCAGCTTTCTTTTATTAATTAATTCCTAT 1587
Db 471 -----AlaTyrSerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGlnAsp 486
QY 1588 AAAATTGGATTAGCGCTAAATATATATATATATACAGTGCATTAGGATGCACACAGTAGT 1647
Db 487 ArgArgGlyThrIle-----ProPhePheThr-----TrpThrHisArgSer 500
QY 1648 GTTAATGAATAATCAATATCAGATAAATAATAATTAATCAATGATCCCAAGCAATCAAGGT 1707
Db 501 ValAspPhePheAsnThrIleAspAlaGluLysIleThrGlnLeuProValValLysAla 520
QY 1708 AACAGTCTTGATACAACTCTAAGGTAAATTCGAAGCACTGCTCATACAGGAGGAACCTTG 1767
Db 521 TyrAlaLeuSerSerGlyAlaSerIleIleGluGlyProGlyPheThrGlyGlyAsnLeu 540

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